10/723552

#1 2-14-06

GAG x Review

Set	Items	Description
S1	3062	GAG()PROTEIN?
S2	2079	RD (unique items)
S3	21	S2 AND REVIEW
S4	526	POL()PROTEIN?
S5	351	RD (unique items)
S6	76	S5 AND ACTIVITY
S7	2	S6 AND REVIEW
S8	1658	ENV()PROTEIN?
S9	1048	RD (unique items)
S10	18	S9 AND REVIEW
S11	166	S9 AND ACTIVITY

? t s3/7/1-21

3/7/1 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

18305994 PMID: 15797210
Structural insights into biological roles of protein-glycosaminoglycan interactions.
Raman Rahul; Sasisekharan V; Sasisekharan Ram
Biological Engineering Division, Massachusetts Institute of Technology, Cambridge, Massachusetts 02139, USA.
Chemistry & biology (England) Mar 2005, 12 (3) p267-77, ISSN 1074-5521 Journal Code: 9500160
Contract/Grant No.: CA 90940; CA; NCI; GM 57073; GM; NIGMS; HL 59966; HL; NHLBI
Publishing Model Print
Document type: Journal Article; Review; Review, Tutorial
Languages: ENGLISH
Main Citation Owner: NLM
Record type: MEDLINE; Completed
The extracellular environment is largely comprised of complex polysaccharides, which were historically considered inert materials that hydrated the cells and contributed to the structural scaffolds. Recent advances in development of sophisticated analytical techniques have brought about a dramatic transformation in understanding the numerous biological roles of these complex polysaccharides. Glycosaminoglycans (GAGs) are a class of these polysaccharides, which bind to a wide variety of proteins and signaling molecules in the cellular environment and modulate their activity, thus impinging on fundamental biological processes. Despite the importance of GAGs modulating biological functions, there are relatively few examples that demonstrate specificity of %%%GAG%%%-%%%protein%%% interactions, which in turn define the structure-function relationships of these polysaccharides. Focusing on heparin/heparan (HSGAGs) and chondroitin/dermatan sulfate (CSGAGs), this %%%review%%% provides structural insights into the oligosaccharide-protein interactions and discusses some key and challenging aspects of understanding GAG structure-function relationships. (60 Refs.)
Record Date Created: 20050330
Record Date Completed: 20050809

3/7/2 (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

16486956 PMID: 15488613
Recombinant HIV-1 Pr55gag virus-like particles: potent stimulators of innate and acquired immune responses.
Deml Ludwig; Speth Cornelia; Dierich Manfred P; Wolf Hans; Wagner Ralf
Institute of Medical Microbiology, University of Regensburg, Franz-Josef-Straurr-Allee 11, D-93053 Regensburg, Germany. ludwig.deml@klinik.uni-regensburg.de
Molecular immunology (England) Feb 2005, 42 (2) p259-77, ISSN

0161-5890 Journal Code: 7905289
Publishing Model Print
Document type: Journal Article; Review; Review, Tutorial
Languages: ENGLISH
Main Citation Owner: NLM
Record type: MEDLINE; Completed
Several previous reports have clearly demonstrated the strong effectiveness of human immunodeficiency virus (HIV) Gag polyprotein-based virus-like particles (VLP) to stimulate humoral and cellular immune responses in complete absence of additional adjuvants. Yet, the mechanisms underlying the strong immunogenicity of these particulate antigens are still not very clear. However, current reports strongly indicate that these VLP act as "danger signals" to trigger the innate immune system and possess potent adjuvant activity to enhance the immunogenicity of per se only weakly immunogenic peptides and proteins. Here, we %%%review%%% the current understanding of how various particle-associated substances and other impurities may contribute to the observed immune-activating properties of these complex immunogens. (102 Refs.)
Record Date Created: 20041018
Record Date Completed: 20050119

3/7/3 (Item 3 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

15357899 PMID: 15168195
HIV-1 assembly and maturation.
Bukrinskaya A G
Program in Molecular Medicine, University of Massachusetts Medical School, 373 Plantation Street, Worcester, MA 01605, U.S.A. Alissa.Bukrinskaya@umassmed.edu
Archives of virology (Austria) Jun 2004, 149 (6) p1067-82, ISSN 0304-8608 Journal Code: 7506870
Publishing Model Print-Electronic
Document type: Journal Article; Review; Review, Tutorial
Languages: ENGLISH
Main Citation Owner: NLM
Record type: MEDLINE; Completed
HIV-1 particles have been studied by structural and chemical approaches, however, the processes of assembly, budding and maturation are just beginning to be characterized, and molecular details of these processes remain poorly defined. This brief %%%review%%% summarizes some recent findings on the final steps of the HIV-1 life cycle and touches upon some unanswered questions, particularly regarding the processes involved in virus maturation and infectivity. (117 Refs.)
Record Date Created: 20040528
Record Date Completed: 20040827
Date of Electronic Publication: 20040305

3/7/4 (Item 4 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

15250333 PMID: 15027003
The molecular basis of HIV capsid assembly--five years of progress.
Adamson Catherine S; Jones Ian M
School of Animal and Microbial Sciences, The University of Reading, Reading RG6 6AJ, UK. c.s.adamson@rdg.ac.uk
Reviews in medical virology (England) Mar-Apr 2004, 14 (2) p107-21, ISSN 1052-9276 Journal Code: 9112448.
Publishing Model Print
Document type: Journal Article; Review; Review, Tutorial
Languages: ENGLISH
Main Citation Owner: NLM
Record type: MEDLINE; Completed
The assembly of HIV is relatively poorly investigated when compared with the process of virus entry. Yet a detailed understanding of the mechanism of assembly is fundamental to our knowledge of the complete life cycle of this virus and also has the potential to inform the development of new

antiviral strategies. The repeated multiple interaction of the basic structural unit, Gag, might first appear to be little more than concentration dependent self-assembly but the precise mechanisms emerging for HIV are far from simple. Gag interacts not only with itself but also with host cell lipids and proteins in an ordered and stepwise manner. It binds both the genomic RNA and the virus envelope protein and must do this at an appropriate time and place within the infected cell. The assembled virus particle must successfully release from the cell surface and, whilst being robust enough for transmission between hosts, must nonetheless be primed for rapid disassembly when infection occurs. Our current understanding of these processes and the domains of Gag involved at each stage is the subject of this %%%review%%%. Copyright 2004 John Wiley & Sons, Ltd. (139 Refs.)
Record Date Created: 20040317
Record Date Completed: 20040506

3/7/5 (Item 5 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

12981983 PMID: 10934287
Mutational analysis of HIV-1 %%%gag%%% %%%proteins%%% (%%%review%%%).
Miyaura M; Yoshida A; Sakurai A; Fujita M; Koyama A H; Adachi A
Department of Virology, The University of Tokushima School of Medicine, Tokushima 770-8503, Japan.
International journal of molecular medicine (GREECE) Sep 2000, 6 (3) p265-9, ISSN 1107-3756 Journal Code: 9810955
Publishing Model Print
Document type: Journal Article; Review; Review, Tutorial
Languages: ENGLISH
Main Citation Owner: NLM
Record type: MEDLINE; Completed
The mature %%%Gag%%% %%%proteins%%% of human immunodeficiency virus type 1 (HIV-1) are major components of infectious virions, and thought to carry out numerous functions throughout the HIV-1 replication cycle. We have recently generated numerous gag gene mutants of HIV-1 to genetically study the functions of the %%%Gag%%% %%%proteins%%%. Through the biological and biochemical analyses, our HIV-1 gag mutants have been grouped into early (defective for uncoating/reverse transcription), late (defective for virion release/maturation), and early/late (defective for both steps) mutants. Many mutants are found to efficiently inhibit the replication of wild-type virus. Worthy of note, there are some early mutants which show host cell-dependent replication potential. (27 Refs.)
Record Date Created: 20000825
Record Date Completed: 20000825

3/7/6 (Item 6 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

12684045 PMID: 10603472
The kelch repeat superfamily of proteins: propellers of cell function.
Adams J; Kelso R; Cooley L
MRC-LMCB and Dept of Biochemistry and Molecular Biology, University College London, Gower Street, London UK.
Trends in cell biology (ENGLAND) Jan 2000, 10 (1) p17-24, ISSN 0962-8924 Journal Code: 9200566
Contract/Grant No.: GM52702; GM; NIGMS
Publishing Model Print
Document type: Journal Article; Review; Review, Tutorial
Languages: ENGLISH
Main Citation Owner: NLM
Record type: MEDLINE; Completed
The kelch motif was discovered as a sixfold tandem element in the sequence of the Drosophila kelch ORF1 protein. The repeated kelch motifs predict a conserved tertiary structure, a beta-propeller. This module appears in many different polypeptide contexts and contains multiple potential protein-protein contact sites. Members of this growing superfamily are present throughout the cell and extracellularly and have

diverse activities. In this %%%review%%%, we discuss current information concerning the structural organization of kelch repeat proteins, their biological roles and the molecular basis of their action. (53 Refs.)
Record Date Created: 20000106
Record Date Completed: 20000106

3/7/7 (Item 7 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

12505066 PMID: 9813197
HIV-1 %%%gag%%% %%%proteins%%% : diverse functions in the virus life cycle.
Freed E O
National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, Maryland, 20892-0460, USA. EFreed@nih.gov
Virology (UNITED STATES) Nov 10 1998, 251 (1) p1-15, ISSN 0042-6822 Journal Code: 0110674
Publishing Model Print
Document type: Journal Article; Review; Review, Tutorial
Languages: ENGLISH
Main Citation Owner: NLM
Record type: MEDLINE; Completed
The %%%Gag%%% %%%proteins%%% of HIV-1, like those of other retroviruses, are necessary and sufficient for the assembly of virus-like particles. The roles played by HIV-1 %%%Gag%%% %%%proteins%%% during the life cycle are numerous and complex, involving not only assembly but also virion maturation after particle release and early postentry steps in virus replication. As the individual Gag domains carry out their diverse functions, they must engage in interactions with themselves, other %%%Gag%%% %%%proteins%%% , other viral proteins, lipid, nucleic acid (DNA and RNA), and host cell proteins. This %%%review%%% briefly summarizes our current understanding of how HIV-1 %%%Gag%%% %%%proteins%%% function in the virus life cycle. (179 Refs.)
Record Date Created: 19981217
Record Date Completed: 19981217

3/7/8 (Item 8 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

12006832 PMID: 9292394
More reliable diagnosis of infection with human immunodeficiency virus type 1 (HIV-1) by detection of antibody IgGs to pol and %%%gag%%% %%%proteins%%% of HIV-1 and p24 antigen of HIV-1 in urine, saliva, and/or serum with highly sensitive and specific enzyme immunoassay (immune complex transfer enzyme immunoassay): a %%%review%%%.
Hashida S; Hashinaka K; Ishikawa S; Ishikawa E
Department of Biochemistry, Miyazaki Medical College, Japan.
Journal of clinical laboratory analysis (UNITED STATES) 1997, 11 (5) p267-86, ISSN 0887-8013 Journal Code: 8801384
Publishing Model Print; Erratum in J Clin Lab Anal 1998;12(1) 76
Document type: Journal Article; Review; Review, Tutorial
Languages: ENGLISH
Main Citation Owner: NLM
Record type: MEDLINE; Completed
Ultrasensitive enzyme immunoassays (immune complex transfer enzyme immunoassays) were developed for antibody IgGs to HIV-1 using recombinant reverse transcriptase (rRT), p17 (rp17), and p24 (rp24) as antigens. Antibody IgGs were reacted with 2,4-dinitrophenyl-recombinant antigens and recombinant antigen-beta-D-galactosidase conjugates, and the immune complexes formed, comprising the three components, were trapped onto polystyrene beads coated with (anti-2,4-dinitrophenyl group) IgG. After washing, the immune complexes were eluted from the polystyrene beads with excess of epsilon N-2,4-dinitrophenyl-L-lysine and were transferred to clean polystyrene beads coated with (antihuman IgG gamma-chain) IgG. beta-D-Galactosidase activity bound to the last polystyrene beads was assayed by fluorometry. By transfer of the immune complexes from one solid phase to another, the nonspecific binding of the beta-D-galactosidase

conjugates was minimized and the sensitivity was markedly improved. The immune complex transfer enzyme immunoassays using rRT, rp17, and rp24 as antigens were 300-1,000-fold, 1,000-3,000-fold, and 30-100-fold, respectively, more sensitive than Western blotting for the corresponding antigens and 10-300-fold more sensitive than a conventional ELISA and a gelatin particle agglutination test. For urine (100 microliters), whole saliva (1 microliter), and serum (1 microliter) samples, the sensitivity and specificity of the immune complex transfer enzyme immunoassay using rRT as antigen were both 100%. However, for urine samples in which the specific activities of antibody IgG to RT, p17, and p24 were much lower than those in serum samples probably due to degradation by the kidney, a longer assay of bound beta-D-galactosidase activity or/and a concentration process for urine was required. The use of more than 1 microliter of whole saliva was recommended for reliable diagnosis of the infections, whereas 1 microliter of serum was sufficient for the purpose. The positivity with rRT as antigen could be confirmed by demonstration of antibody IgGs to p17 and p24 in most of the urine, whole saliva, and serum samples. In HIV-1 seroconversion serum panels, antibody IgG to p17 was detected as early as or even earlier than antibodies to HIV-1 by a conventional ELISA or/and a gelation particle agglutination test, whereas antibody IgGs to RT and p24 were detected as early as or later than antibody IgG to p17. Thus the uses of rRT and rp17 as antigens were advantageous over that of the other antigens for randomly collected serum samples probably long after the infection and serum samples at early stages of the infection, respectively. On the basis of these results and other reports, the immune complex transfer enzyme immunoassay was developed for simultaneous detection of p24 antigen and antibody IgGs to RT and p17 in a single assay tube, and the window period (8 weeks, although widely variable), during which diagnosis of HIV-1 infection is not possible due to the absence of detectable antibodies to HIV-1, was shortened by 2 weeks. As a result, the simultaneous detection made possible not only as early diagnosis as that by detection of p24 antigen, but also as reliable diagnosis as that by detection of antibodies to HIV-1. Finally, the immune complex transfer enzyme immunoassay has been recently improved so as to be performed within shorter periods of time (2-3 hr) with higher sensitivity, and testing many samples has become easy. (62 Refs.)
Record Date Created: 19971027
Record Date Completed: 19971027

3/7/9 (Item 9 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

11667430 PMID: 8982451
Prions and RNA viruses of Saccharomyces cerevisiae.
Wickner R B
National Institute of Diabetes, Digestive and Kidney Disease, National Institute of Health, Bethesda, Maryland 20892-0830, USA.
Annual review of genetics (UNITED STATES) 1996, 30 p109-39, ISSN 0066-4197 Journal Code: 0117605
Publishing Model Print
Document type: Journal Article; Review
Languages: ENGLISH
Main Citation Owner: NLM
Record type: MEDLINE; Completed
Saccharomyces cerevisiae is host to the dsRNA viruses L-A (including its killer toxin-encoding satellite, M) and L-BC, the 20S and 23S ssRNA replicons, and the putative prions, [URE3] and [PSI]. %%%review%%% the genetic and biochemical evidence indicating that [URE3] and [PSI] are prion forms of Ure2p and Sup35p, respectively. Each has an N-terminal domain involved in propagation or generation of the prion state and a C-terminal domain responsible for the protein's normal function, nitrogen regulation, or translation termination, respectively. The L-A dsRNA virus expression, replication, and RNA packaging are reviewed. L-A uses a -1 ribosomal frameshift to produce a Gag-Pol fusion protein. The host SK12, SK13 and SK18 proteins block translation of nonpoly(A) mRNAs (such as viral mRNA). Mutants deficient in 60S ribosomal subunits replicate L-A poorly, but not if cells are also ski-. Interaction of 60S subunits with the 3' polyA is suggested. SKI1/XRN1 is a 5'--> 3' exoribonuclease that degrades uncapped mRNAs. The viral %%%Gag%%% %%%protein%%% decapitates cellular mRNAs apparently to decoy this enzyme from working on viral mRNA. (141 Refs.)

Record Date Created: 19970318
Record Date Completed: 19970318

3/7/10 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0014508834 BIOSIS NO.: 200300464445
Role of HIV-1 Gag domains in viral assembly.
AUTHOR: Scarlata Suzanne (Reprint); Carter Carol
AUTHOR ADDRESS: Department of Physiology and Biophysics, State University of New York at Stony Brook, Stony Brook, NY, 11794-8661, USA**USA
AUTHOR E-MAIL ADDRESS: suzanne@dualphy.pnb.sunysb.edu
JOURNAL: Biochimica et Biophysica Acta 1614 (1): p62-72 11 July, 2003 2003
MEDIUM: print
ISSN: 0006-3002 _(ISSN print)
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: After entry of the human immunodeficiency virus type 1 (HIV-1) into T cells and the subsequent synthesis of viral products, viral proteins and RNA must somehow find each other in the host cells and assemble on the plasma membrane to form the budding viral particle. In this general %%%review%%% of HIV-1 assembly, we present a brief overview of the HIV life cycle and then discuss assembly of the HIV Gag polyprotein on RNA and membrane substrates from a biochemical perspective. The role of the domains of Gag in targeting to the plasma membrane and the role of the cellular host protein cyclophilin are also reviewed.

3/7/11 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0014172511 BIOSIS NO.: 200300131230
Advances in HIV molecular biology.
AUTHOR: Gummuluru Suryaram; Emerman Michael (Reprint)
AUTHOR ADDRESS: Fred Hutchinson Cancer Research Center, 1100 Fairview Ave. N., Mail-stop C2-023, P.O. Box 19024, Seattle, WA, 98109-1024, USA**USA
AUTHOR E-MAIL ADDRESS: memerman@fhcrc.org
JOURNAL: AIDS (Hagerstown) 16 (Supplement 4): pS17-S23 2002 2002
MEDIUM: print
ISSN: 0269-9370
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Citation
LANGUAGE: English

3/7/12 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0013715378 BIOSIS NO.: 200200308889
Viral late domains
AUTHOR: Freed Eric O (Reprint)
AUTHOR ADDRESS: NIAID, NIH, Bldg. 4, Rm. 307, Bethesda, MD, 20892-0460, USA **USA
JOURNAL: Journal of Virology 76 (10): p4679-4687 May, 2002 2002
MEDIUM: print
ISSN: 0022-538X
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Citation
LANGUAGE: English

3/7/13 (Item 4 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0013669026 BIOSIS NO.: 200200262537
Human immunodeficiency virus nucleocapsid protein polymorphisms modulate the infectivity of RNA packaging mutants
AUTHOR: Krogstad Paul (Reprint); Geng Yong-Zhi; Rey Osvaldo; Canon Jude; Ibarrondo F Javier; Ackerson Bradley; Patel Jignesh; Aldovini Anna
AUTHOR ADDRESS: Departments of Pediatrics and Molecular and Medical Pharmacology, UCLA School of Medicine, 10833 Le Conte Ave., Los Angeles, CA, 90095, USA**USA
JOURNAL: Virology 294 (2): p282-288 March 15, 2002 2002
MEDIUM: print
ISSN: 0042-6822
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The nucleocapsid protein (NC) of retroviruses is involved in viral RNA packaging and initiation of reverse transcription. NC also mediates interactions between Gag and actin filaments. We found that residues at the amino terminus of NC are involved in efficient actin binding. When alanine residues were substituted for the arginine and lysine at positions 10 and 11 of NC in HIVNL4-3, these mutations decreased actin binding but had only a modest effect on virus infectivity. A similarly mutated virus based on the HXB2 clone of HIV was not infectious. Mutational analysis of NL4-3 NC residues demonstrated that NC polymorphisms modulated the phenotype of NC mutations. Conservative amino acid differences between HXB2 and NL4-3 NCs were sufficient to explain the difference in infectivity of viruses carrying the R10A and K11A mutations.

3/7/14 (Item 5 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0012987032 BIOSIS NO.: 200100158871
Identification of highly conserved and broadly cross-reactive HIV type 1 cytotoxic T lymphocyte epitopes as candidate immunogens for inclusion in Mycobacterium bovis BCG-vectored HIV vaccines
AUTHOR: Ferrari Guido (Reprint); Kostyu Donna D; Cox Josephine; Dawson Deborah V; Flores Jorge; Weinhold Kent J; Osmanov Saladin
AUTHOR ADDRESS: Department of Surgery, Duke University Medical Center, DUMC 2926, LaSalle St. Ext, SORF Bldg., Durham, NC, 27710, USA**USA
JOURNAL: AIDS Research and Human Retroviruses 16 (14): p1433-1443 September 20, 2000 2000
MEDIUM: print
ISSN: 0889-2229
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: One of the fundamental goals of current strategies to develop an efficacious vaccine for AIDS is the elicitation of cytotoxic T lymphocyte (CTL) reactivities capable of recognizing cells infected with different subtypes of the human immunodeficiency virus type 1 (HIV-1). In efforts to explore new vaccine candidates by the UNAIDS/WHO Vaccine Committee, we %%%review%%% the most recent data concerning CTL epitopes that are conserved among the different HIV-1 subtypes. Moreover, we examine HLA allelic frequencies in several different populations, to determine those that could contribute to the goal of a cumulative phenotype frequency (CP) of at least 80%. By analyzing conserved epitopes in the context of HLA restricting alleles, we define a set of HIV-1 gene regions that may have the greatest potential to induce cross-clade reactive CTLs. The absence of well-defined correlates of immune protection that link CTL epitopes to delayed disease progression and/or prevention of infection does not permit an assignment of rank order of the most relevant component of a candidate vaccine. Thus far, most of the studies conducted in clade B-infected patients to define conserved and immunodominant epitopes indicate gag and pol gene products to be the most conserved among the HIV-1 subtypes. Moreover, anti-Pol and -Gag CTL responses appear to correlate inversely with disease progression, suggesting that

they should be among the first choice of antigens to be included in a candidate vaccine construct aimed at induction of broad CTL responses. The impact of a clade B-based vaccine as a worldwide candidate capable of inducing protective immune responses can be determined only after "in vivo" studies. Meanwhile, extensive parallel studies in populations infected with non-clade B HIV-1 subtypes should define the patterns of immunodominant epitopes and HLA for comparison with the data already collected in clade B-infected subjects.

3/7/15 (Item 6 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0011905689 BIOSIS NO.: 199900165349
Foamy viruses are unconventional retroviruses
AUTHOR: Linial Maxine L (Reprint)
AUTHOR ADDRESS: Div. Basic Sci., Fred Hutchinson Cancer Res. Cent., 1100 Fairview Ave. N., Seattle, WA 98109, USA**USA
JOURNAL: Journal of Virology 73 (3): p1747-1755 March, 1999 1999
MEDIUM: print
ISSN: 0022-538X
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Citation
LANGUAGE: English

3/7/16 (Item 7 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0011578830 BIOSIS NO.: 199800373077
The molecular basis of HIV capsid assembly
AUTHOR: Jones Ian M (Reprint); Morikawa Yuko
AUTHOR ADDRESS: NERC Inst. Virol., Mansfield Road, Oxford OX1 3SR, UK**UK
JOURNAL: Reviews in Medical Virology 8 (2): p87-95 April-June, 1998 1998
MEDIUM: print
ISSN: 1052-9276
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Citation
LANGUAGE: English

3/7/17 (Item 8 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0011578390 BIOSIS NO.: 199800372637
Retroviral matrix proteins: A structural perspective
AUTHOR: Conte Maria R; Matthews Stephen (Reprint)
AUTHOR ADDRESS: Dep. Biochemistry, Imperial College Science, Techol. Med., Exhibition Road, South Kensington, London SW7 2AY, UK**UK
JOURNAL: Virology 246 (2): p191-198 July 5, 1998 1998
MEDIUM: print
ISSN: 0042-6822
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Citation
LANGUAGE: English

3/7/18 (Item 9 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0011113749 BIOSIS NO.: 199799747809
Electrostatic interaction of myristoylated proteins with membranes: Simple physics, complicated biology
AUTHOR: Murray Diana; Ben-Tal Nir; Honig Barry; McLaughlin Stuart (Reprint)
AUTHOR ADDRESS: Dep. Physiol. Biophysics, SUNY Stony Brook, Stony Brook, NY 11794-8661, USA**USA
JOURNAL: Structure (London) 5 (8): p985-989 1997 1997

ISSN: 0969-2126
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Cell membrane association by several important peripheral proteins, such as Src, MARCKS, HIV-1 Gag, an K-Ras, requires nonspecific electrostatic interactions between a cluster of basic residues on the protein and acidic phospholipids in the plasma membrane. A simple theoretical model based on the nonlinear Poisson-Boltzmann equation describes well the experimentally measured electrostatic association between such proteins and the cell membrane.

3/7/19 (Item 10 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0010134797 BIOSIS NO.: 199698602630
Proteins of bovine leukemia virus and human T-cell leukemia viruses
AUTHOR: Hruskova-Heidingsfeldova O
AUTHOR ADDRESS: Dep. Biochem., Inst. Organic Chem. Biochem., Acad. Sci. Czech Republic, 166 10, Praha 6, Czech Republic**Czech Republic
JOURNAL: Folia Biologica (Prague) 41 (5): p201-212 1995 1995
ISSN: 0015-5500
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Citation
LANGUAGE: English

3/7/20 (Item 11 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0008449987 BIOSIS NO.: 199344012882
HLA class I binding regions of HIV-1 proteins
AUTHOR: Choppin Jeannine; Guillet Jean-Gerard; Levy Jean-Paul
AUTHOR ADDRESS: Inst. Cochin Genetique Moleculaire, INSERM U. 152, 27 rue du Faubourg Saint-Jacques, 75014 Paris, France**France
JOURNAL: Critical Reviews in Immunology 12 (1-2): p1-16 1992
ISSN: 1040-8401
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Citation
LANGUAGE: English

3/7/21 (Item 12 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0003396882 BIOSIS NO.: 198222040825
STRUCTURE AND PROPERTIES OF PROTEINS OF RETROVIRUS TYPE C
AUTHOR: MAZURENKO N N (Reprint)
AUTHOR ADDRESS: ONCOL SCI CENT, ACAD MED SCI USSR, MOSCOW, USSR**USSR
JOURNAL: Voprosy Virusologii (6): p644-654 1980
ISSN: 0507-4088
DOCUMENT TYPE: Article
RECORD TYPE: Citation
LANGUAGE: RUSSIAN

? t s2/7/2070-2079

2/7/2070 (Item 566 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0002471774 BIOSIS NO.: 197866058258
CELL-FREE SYNTHESIS OF RAUSCHER MURINE LEUKEMIA VIRUS GAG AND GAG-POL PRECURSOR POLY PROTEINS FORM VIRION 35S RNA IN A MESSENGER RNA DEPENDENT TRANSLATION SYSTEM DERIVED FROM MOUSE TISSUE CULTURE CELLS

AUTHOR: MURPHY E C JR (Reprint); ARLINGHAUS R B
AUTHOR ADDRESS: DEP BIOL, UNIV TEX SYST CANCER CENT, MD ANDERSON HOSP TUMOR INST, HOUSTON, TEX 77030, USA**USA
JOURNAL: Virology 86 (2): p329-343 1978
ISSN: 0042-6822
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Using a mRNA-dependent cell-free protein synthesis system derived from mouse tissue culture cell extracts by treatment with micrococcal nuclease, the capacity of 35S genomic RNA from Rauscher leukemia virus (RLV) to code for the synthesis of viral proteins was examined. Analysis of the polypeptide product by SDS[sodium dodecyl chamber]-polyacrylamide gel electrophoresis (PAGE) indicated that RLV 35S RNA directed the synthesis of RLV-specific polypeptides of 55,000, 65,000, 75,000 and 200,000 apparent MW, identical in size to the known intracellular precursors of the RLV mature polypeptides. None of the individual mature virus proteins appeared to be synthesized. If canavanine, an arginine analog, was substituted for arginine under conditions for cell-free protein synthesis, a RLV-specific polypeptide with a MW of approximately 80,000 was synthesized at the expense of the 65,000 and 75,000 MW polypeptides. Monospecific antisera directed against p30, p15, p12 and p10 recognized the 65,000, 75,000 80,000 and 200,000 MW polypeptides, indicating that each shared antigenic determinants with all of these %%%gag%%% %%%proteins%%%. Using the appropriate authentic RLV precursor polypeptides as standards, comparative tryptic maps were performed with the [3H]tyrosine or [35S]methionine-labeled in vitro-synthesized 65,000 and 200,000 MW polypeptides. The 65,000 MW polypeptide was identical to Pr65gag,2 a 65,000 MW RLV %%%gag%%% %%%protein%%% precursor obtained from infected cells by immunoprecipitation and gel electrophoresis. The 20,000 MW in vitro synthesized polypeptide contained methionine-labeled tryptic peptides characteristic of the RLV reverse transcriptase (pol) and p30.

2/7/2071 (Item 567 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0002471746 BIOSIS NO.: 197866058230
PROTEINS OF ROUS ASSOCIATED VIRUS 61 AND AVIAN RETROVIRUS COMMON PRECURSOR FOR GLYCO PROTEIN 85 AND GLYCO PROTEIN 35 AND USE OF PACTAMYCIN TO MAP TRANSLATIONAL ORDER OF PROTEINS IN THE GAG POL AND ENV GENES
AUTHOR: SHEALY D J (Reprint); RUECKERT R R
AUTHOR ADDRESS: BIOCHEM DEP, COLL AGRIC LIFE SCI, UNIV WIS, MADISON, WIS 53706, USA**USA
JOURNAL: Journal of Virology 26 (2): p380-388 1978
ISSN: 0022-538X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Cells [chick embryo] infected by Rous-associated virus 61 (RAV-61) contained a precursor-like protein, pr90, that was specifically precipitated by antiserum directed against envelope glycoproteins, gp85 and gp35. Tryptic peptide mapping showed that pr90 contained tryptic sequences of both gp85 and gp35. Pactamycin mapping experiments indicated that the 2 glycoproteins are translated from the env-mRNA in the order (5') gp85-gp35. The pactamycin mapping experiments also indicated a translational order of p19-(p27, p12)-p15 for the %%%gag%%% %%%proteins%%%; this agreement with the order previously reported from tryptic mapping studies on precursor pr76 of avian myeloblastosis virus implied that the stoichiometry of the core proteins was unchanged when virions were assembled in the presence of pactamycin. The reverse transcriptase proteins, unlike those of the env and gag genes, fell on the right side of the pactamycin map. Apparently most, if not all, of the reverse transcriptase protein is translated by read-through of the gag(pol) message rather than by translation of a hypothetical pol-mRNA devoted solely to synthesis of that protein.

2/7/2072 (Item 568 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0002463128 BIOSIS NO.: 197866049612
VIRAL POLY PROTEINS IN CHICK EMBRYO FIBROBLASTS INFECTED WITH AVIAN SARCOMA LEUKOSIS VIRUSES
AUTHOR: HAYMAN M J (Reprint)
AUTHOR ADDRESS: IMP CANCER RES FUND, PO BOX 123, LINCOLN'S INN FIELDS, LONDON WC2A 3PX, ENGL, UK**UK
JOURNAL: Virology 85 (1): p241-252 1978
ISSN: 0042-6822
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Chicken embryo fibroblasts infected by avian RNA tumor viruses were analyzed by immune precipitation for the synthesis of virus-specific proteins. Three virus-specific precursor polyproteins with MW of 180,000, 95,000 and 76,000 were detected following pulse-labeling of the cells. The 76,000 dalton polyprotein is the precursor to the nonglycosylated %%%gag%%% %%%proteins%%% of the virion as shown earlier. By using monospecific antisera it was possible to identify the 180,000 dalton polyprotein as having sequences in common with the virion polymerase and the gag and the 95,000 dalton polyprotein as being related to the virion glycoproteins gp85 and gp37. Although the 180,000 dalton protein contains sequences for the %%%gag%%% %%%proteins%%%, pulse-chase experiments indicated that it did not represent a precursor to the major 76,000 dalton gag precursor polyprotein and is most likely synthesized by an occasional read-through of the mRNA for the gag precursor polyprotein.

2/7/2073 (Item 569 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0002444540 BIOSIS NO.: 197866031024
BIOSYNTHESIS OF REVERSE TRANSCRIPTASE FROM RAUSCHER MURINE LEUKEMIA VIRUS BY SYNTHESIS AND CLEAVAGE OF A GAG-POL READ-THROUGH VIRAL PRECURSOR POLY PROTEIN
AUTHOR: KOPCHICK J J (Reprint); JAMJOOM G A; WATSON K F; ARLINGHAUS R B
AUTHOR ADDRESS: DEP BIOL, UNIV TEX SYST CANCER CENT, MD ANDERSON HOSP TUMOR INST, HOUSTON, TEX 77030, USA**USA
JOURNAL: Proceedings of the National Academy of Sciences of the United States of America 75 (4): p2016-2020 1978
ISSN: 0027-8424
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Reverse transcriptase (RT; RNA-dependent DNA nucleotidyltransferase) from Rauscher leukemia virus is synthesized in infected [mouse] cells by way of a read-through polyprotein of 200,000 MW. This polyprotein (Pr200gag-pol) was precipitated by antiserum to RT; in a previous study all the monospecific antisera to %%%gag%%% %%%proteins%%% recognized Pr200gag-pol. Pr200gag-pol contains both p30 and RT peptide sequences. Intermediate RT-related precursors of 145,000 (Pr145pol), 135,000 (Pr135pol) and 125,000 (Pr125pol) MW were specifically recognized by precipitation from infected cell extracts by antiserum to RT. These proteins shared methionine-containing tryptic peptide sequences with a virion polypeptide of 80,000 MW (p80pol) precipitable by antiserum to RT. Purification of active RT enzyme from virions labeled with [3H]methionine showed that p80pol was the major component, based on analysis by gel electrophoresis and tryptic peptide mapping experiments. A polypeptide (Pr80pol), similar in size to mature viral p80pol, was also precipitated from infected cells by antiserum to RT. Its peptide map was nearly identical to that of virion p80pol. Pulse-chase studies showed that Pr80pol, Pr125pol, and Pr135pol were stable polypeptides, but Pr200gag-pol and Pr145pol were unstable precursors. Pulse-chase studies with the protein synthesis inhibitor, cycloheximide, showed that the processing of Pr200gag-pol occurred for a

short time in the absence of protein synthesis.

2/7/2074 (Item 570 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0002421774 BIOSIS NO.: 197866008258
CELL-FREE SYNTHESIS OF A PRECURSOR POLY PROTEIN CONTAINING BOTH GAG AND POL GENE PRODUCTS BY RAUSCHER MURINE LEUKEMIA VIRUS 35S RNA
AUTHOR: MURPHY E C JR (Reprint); KOPCHICK J J; WATSON K F; ARLINGHAUS R B
AUTHOR ADDRESS: DEP BIOL, UNIV TEX SYST CANCER CENT, MD ANDERSON HOSP TUMOR INST, HOUSTON, TEX 77030, USA**USA
JOURNAL: Cell 13 (2): p359-370 1978
ISSN: 0092-8674
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Translation of Rauscher murine leukemia virus (RLV) 35S RNA in a mRNA-dependent protein-synthesizing system results in the synthesis of polypeptides with apparent MW of 200,000, 75,000 and 65,000 daltons. Each of these polypeptides was immunoprecipitable with anti-p30 serum, while only the 200,000 dalton size class was specifically recognized by antiserum prepared against purified reverse transcriptase. Intracellular Pr200gag-pol contained p30 tryptic peptide sequences and shared antigenic determinants with the %%%gag%%% %%%proteins%%% p30, p15, p12 and p10 and the reverse transcriptase. These results and others showed that Pr200gag-pol is the initial translation product that leads to the formation of mature reverse transcriptase. In the present study, 9 of 11 methionine-containing tryptic peptides found in an anti-reverse transcriptase-precipitable 80,000 dalton MW virion polypeptide (p80pol) were contained in Pr200gag-pol. Virion p80pol co-migrates in SDS[sodium dodecyl sulfate]-polyacrylamide gels with the major polypeptide found in partially purified preparations of active reverse transcriptase. The in vitro synthesized 200,000 dalton polypeptide was identical to intracellular Pr200gag-pol as determined by comparing ion-exchange profiles of methionine-labeled tryptic peptides. The frequency of synthesis of the in vitro synthesized Pr200gag-pol was 1/25-1/20 that of the combined synthesis of the 65,000 and 75,000 dalton gag precursors. A similar ratio of Pr200gag-pol to Pr65gag and Pr80gag was observed in viral infected [mouse] cells. Thus 35S viral genomic RNA is an mRNA for both gag and pol gene products. Experiments with the arginine analog canavanine suggest that the usual termination signal occurs after the translation of Pr80gag. The Pr200gag-pol probably results from an occasional read-through (5% frequency) of a single termination codon at the end of the gag gene.

2/7/2075 (Item 571 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0002403082 BIOSIS NO.: 197865064069
MOLECULAR MECHANISMS INVOLVED IN THE DIFFERENTIAL EXPRESSION OF GAG GENE PRODUCTS BY CLONAL ISOLATES OF A PRIMATE SARCOMA VIRUS
AUTHOR: ROBBINS K C (Reprint); OKABE H; TRONICK S R; GILDEN R V; AARONSON S A
AUTHOR ADDRESS: LAB RNA TUMOR VIRUSES, NATL CANCER INST, BETHESDA, MD 20014, USA**USA
JOURNAL: Journal of Virology 25 (2): p471-478 1978
ISSN: 0022-538X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Clonal isolates of an early passage stock of woolly monkey sarcoma virus (WSV) coded for different numbers of woolly monkey helper leukemia virus gag gene products. The molecular mechanisms responsible for their differential expression of gag gene products were analyzed. Three WSV RNA genomes possessed sedimentation coefficients consistent

with the differences demonstrated in their allotments of helper viral sequences. The WSV variant (WSV clone 9) that expressed no detectable proteins contained the largest amount of helper viral information. There was no additive hybridization of the WLV complementary DNA probe by RNA of this WSV clone and that of a WSV clone coding for several gag gene products. The lack of expression of gag gene products by WSV clone 9 is probably not due to a major deletion of helper viral gag gene sequences. Similar levels of WLV-specific RNA were demonstrated in [human and rat] cells nonproductively transformed by each WSV clone, arguing that the ability to express %%%gag%%% %%%proteins%%% was not related to the magnitude of viral RNA transcription. Taken together, the results are most consistent with a mechanism by which small deletions or point mutations in the genomes of some WSV variants result in premature termination of translation or synthesis of immunologically nonreactive gag gene proteins. The present findings have implications concerning the effects of evolutionary selective pressures on helper viral genetic information in mammalian transforming viruses.

2/7/2076 (Item 572 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0002388613 BIOSIS NO.: 197865049600
GAG POLY PROTEIN PRECURSORS OF RAUSCHER MURINE LEUKEMIA VIRUS
AUTHOR: ARCEMENT L J (Reprint); KARSHIN W L; NASO R B; ARLINGHAUS R B
AUTHOR ADDRESS: DEP BIOL, UNIV TEX SYST CANCER CENT, MD ANDERSON HOSP TUMOR INST, HOUSTON, TEX 77030, USA**USA
JOURNAL: Virology 81 (2): p284-297 1977
ISSN: 0042-6822
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The major polyprotein precursors of the 4 internal structural proteins of Rauscher murine leukemia virus, designated p30, p15, p12 and p10 (collectively termed %%%gag%%% %%%proteins%%%), were characterized. Tryptic peptide sequences and antigenic determinants of the %%%gag%%% %%%proteins%%% are contained in precursor polyproteins Pr3 (.simeq. 80,000) and Pr4 (.simeq. 65,000 daltons). Two main precursor polyproteins were also identified and partially characterized. They are designated Pr5 (.simeq. 55,000) and Pr6 (.simeq. 45,000 daltons). Pr5 contains peptide sequences of p30, p15 and p12; Pr6 contains sequences of p30 and p12 but lacks p15 sequences. The presence or absence of p10 sequences in Pr5 and Pr6 remains to be established. The major pathways for formation of the %%%gag%%% %%%proteins%%% appears to be via synthesis and processing of Pr3. Antigenic determinants of the %%%gag%%% %%%proteins%%% (and p30 peptide sequences) are also contained in a polyprotein precursor termed Pr1a+b (MW, .simeq. 200,000). The latter shared antigenic determinants with the reverse transcriptase.

2/7/2077 (Item 573 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0002382359 BIOSIS NO.: 197865043346
SYNTHESIS AND GLYCOSYLATION OF POLY PROTEIN PRECURSORS TO THE INTERNAL CORE PROTEINS OF FRIEND MURINE LEUKEMIA VIRUS
AUTHOR: EVANS L H (Reprint); DRESLER S; KABAT D
AUTHOR ADDRESS: DEP BIOCHEM, SCH MED, UNIV OREG HEALTH SCI CENT, PORTLAND, OREG 97201, USA**USA
JOURNAL: Journal of Virology 24 (3): p865-874 1977
ISSN: 0022-538X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Synthesis and post-translational processing of murine leukemia virus proteins were analyzed in a murine [mouse embryo] cell line (Eveline) that produces large amounts of Friend lymphatic leukemia virus.

Immunoprecipitation of L-[35S]methionine-labeled cell extracts demonstrated that several different virus-specific proteins antigenically related to the virion core (%%%gag%%%) %%%proteins%%% p12 and p30 become radioactive within 1 min of labeling and exhibit labeling kinetics characteristic of primary translation products. The most abundant of these were proteins with MW of 75,000 and 65,000. There also were 2 large glycosylated polyproteins with apparent MW of 220,000 and 230,000, which were precipitated by antisera to p30 or p12 but not by antiserum to the major envelope glycoproteins gp69/71. Several lines of evidence, including labeling with D-[3H]glucosamine and binding to insolubilized lectins, suggested that the 75,000 dalton internal core polyprotein is slowly processed to form a glycoprotein with an apparent MW of 93,000. The 65,000 dalton protein appeared to be an immediate precursor to the virion core proteins. Its processing can involve intermediates containing p30 and p12 antigens with MW of 50,000 and 40,000, but the latter did not appear to be obligatory intermediates. The detection of the 40,000 dalton protein suggested that the genes for p30 and p12 are adjacent on the viral genome. Apparently, there are several pathways of synthesis and post-translational processing of polyprotein precursors to the %%%gag%%% %%%proteins%%% and several of these polyproteins are glycosylated. A comparison of gag precursor processing in rapidly growing, slowly growing and stationary cells indicated that different pathways are favored under different conditions of cell growth. The analysis of envelope glycoprotein synthesis confirmed the existence of 2 rapidly labeled 90,000 dalton glycoproteins, which appear to be precursors to the envelope glycoproteins gp69/71.

2/7/2078 (Item 574 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0002372337 BIOSIS NO.: 197865033324
CELL-FREE SYNTHESIS OF THE PRECURSOR POLY PEPTIDE FOR AVIAN MYELOBLASTOSIS VIRUS DNA POLYMERASE EC-2.7.7.7
AUTHOR: PATERSON B M (Reprint); MARCIANI D J; PAPAS T S
AUTHOR ADDRESS: LAB BIOCHEM, NATL CANCER INST, BETHESDA, MD 20014, USA**USA
JOURNAL: Proceedings of the National Academy of Sciences of the United States of America 74 (11): p4951-4954 1977
ISSN: 0027-8424
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: High MW RNA (35S) isolated from avian myeloblastosis virus directs the cell-free synthesis of 2 prominent polypeptides of 180,000 and 76,000 MW. The latter polypeptide was previously identified as the precursor to the group-specific antigens of the virus (%%%gag%%% %%%proteins%%%). Two-dimensional tryptic peptide analyses of the [35S]methionine-labeled peptides demonstrate that the 180,000 dalton product is a polyprotein that can account for all the peptides of the avian myeloblastosis virus DNA polymerase (DNA nucleotidyltransferase, EC 2.7.7.7.) and those of the gag viral proteins. This is direct confirmation of the genomic order of the viral structural genes, placing the polymerase gene adjacent to the 5'-proximal gag gene of the virus. The primary polymerase gene product is probably the .beta. subunit of the enzyme. These results are discussed in relation to the proposed structural gene map for the avian retraviruses and suggest a model for the in vivo processing of the viral polymerase.

2/7/2079 (Item 575 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0002023892 BIOSIS NO.: 197713049884
EFFECT OF INTERFERON ON THE SYNTHESIS OF INTRA CELLULAR RAUSCHER LEUKEMIA VIRUS PRECURSOR PROTEINS
AUTHOR: CHANG Y-H; NASO R B
JOURNAL: Abstracts of the Annual Meeting of the American Society for Microbiology 77 p290 1977

ISSN: 0094-8519
DOCUMENT TYPE: Article
RECORD TYPE: Citation
LANGUAGE: Unspecified

Pol x Activity

? t s6/7/70-76

6/7/70 (Item 17 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0010227114 BIOSIS NO.: 199698694947
A transient precursor of the HIV-1 protease: Isolation, characterization, and kinetics of maturation
AUTHOR: Wondrak Ewald M; Nashed Nashaat T; Haber Martin T; Jerina Donald M; Louis John M (Reprint)
AUTHOR ADDRESS: Building 6, Room B1-16, NIDDK, National Inst. Health, Bethesda, MD 20892, USA**USA
JOURNAL: Journal of Biological Chemistry 271 (8): p4477-4481 1996 1996
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Recently, the mechanism of autoprocessing of the protease (PR) of the human immunodeficiency virus type 1 from the model polyprotein, MBP-DELTA-TF-PR-DELTA-Pol, which contains the protease linked to short native flanking sequences (DELTA-TF and DELTA-Pol) fused to the maltose binding protein (MBP) of Escherichia coli, was reported (Louis, J. M., Nashed, N. T., Parris, K. D., Kimmel, A. R., and Jerina, D. M. (1994) Proc. Natl. Acad. Sci. U. S. A. 91, 7970-7974). According to this mechanism, intramolecular cleavage of the N-terminal strands of the dimeric MBP-DELTA-TF-PR-DELTA-%%%Pol%%% %%%protein%%% leads to the formation of the PR-DELTA-Pol intermediate, which is subsequently converted to the mature protease by cleavage of the C-terminal strands. We now report the purification and characterization of the PR-DELTA-Pol intermediate and the kinetics of its processing to the mature protease. Unlike the MBP-DELTA-TF-PR-DELTA-Pol precursor, PR-DELTA-pol has proteolytic %%%activity%%% similar to that of the mature enzyme at Ph 5.0. The pH rate profile for k-cat/K-m is similar to that of the mature protease above pH 4.0. Although the PR-DELTA-pol is more sensitive than the mature protease toward denaturing reagents, both the enzymatic %%%activity%%% and the intrinsic fluorescence of PR-DELTA-pol are linearly dependent on the protein concentration, indicating that the protein is largely in its dimeric form above 10 nM. In contrast to the first-order kinetics observed for the proteolytic reaction at the N terminus of the protease, the proteolytic reaction at the C terminus of the protease is second order in protein concentration. These results are discussed in terms of a mechanism in which the C-terminally located DELTA-pol peptide chains are cleaved intermolecularly to release the mature protease.

6/7/71 (Item 18 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0009983337 BIOSIS NO.: 199598451170
Elongation %%%activity%%% of poliovirus RNA polymerase derived from Sabin type 1 sequence is not temperature sensitive
AUTHOR: Baker Susan; Richards Oliver C; Ehrenfeld Ellie (Reprint)
AUTHOR ADDRESS: Dep. Molecular Biol. Biochem., Univ. California Irvine, Irvine, CA 92717, USA**USA
JOURNAL: Journal of General Virology 76 (8): p2081-2084 1995 1995
ISSN: 0022-1317
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Determinants of attenuation in the Sabin type 1 strain of

poliovirus are located in the 5' noncoding region, the capsid coding region and the viral RNA-dependent RNA polymerase (3D-pol) coding region. These mutations also contribute to a temperature sensitive phenotype of virus replication. We have cloned and expressed the Sabin 1 virus 3D-%%%pol%%% %%%protein%%% which contains three amino acid differences from the wild-type (Mahoney) sequence, as well as a wild-type polymerase containing only a single Sabin amino acid substitution at nt 6203. These enzymes have been examined and compared for temperature sensitive polymerase %%%activity%%%. Wild-type and mutated polymerases demonstrated identical specific activities at 30, 35 and 39 degree C. All three showed the same kinetics of heat inactivation after pre-incubation at elevated temperatures. Thus the contribution of Sabin 3D-pol sequences to the inability of the virus to grow at elevated temperatures must lie in a function or %%%activity%%% of the enzyme other than RNA polymerization. A likely reaction is the initiation step of RNA chain synthesis.

6/7/72 (Item 19 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0009019696 BIOSIS NO.: 199497040981
Picornavirus nonstructural proteins: Emerging roles in virus replication and inhibition of host cell functions
AUTHOR: Porter Alan G
AUTHOR ADDRESS: Inst. Mol. Cell Biol., Natl. Univ. Singapore, 10 Kent Ridge Crescent, Singapore 0511, Singapore**Singapore
JOURNAL: Journal of Virology 67 (12): p6917-6921 1993 1993
ISSN: 0022-538X
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Citation
LANGUAGE: English

6/7/73 (Item 20 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0008967145 BIOSIS NO.: 199396131561
Expression of poliovirus P3 proteins using a recombinant vaccinia virus results in proteolytically active 3CD precursor protein without further processing to 3C-pro and 3D-pol
AUTHOR: Porter Donna C; Ansardi David C; Lentz Michael R; Morrow Casey D (Reprint)
AUTHOR ADDRESS: Dep. Microbiology, Univ. Ala. at Birmingham, Birmingham, AL 35294, USA**USA
JOURNAL: Virus Research 29 (3): p241-254 1993
ISSN: 0168-1702
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The expression of the poliovirus genome occurs by the translation of a single open reading frame to generate a long polyprotein which is subsequently processed by viral encoded proteases. The initial proteolytic cleavages result in the production of a P1 polyprotein which contains the capsid proteins, and the P2 and P3 polyproteins which contain proteins required for replication. The P3 polyprotein consists of the 3AB protein (containing the viral genome-linked protein, VPg), the viral protease, 3C-pro, and RNA polymerase, 3D-pol. To further study the expression and proteolytic processing of poliovirus P3 proteins in vivo, we have utilized recombinant vaccinia virus vectors to express nucleotides 5240-7400 containing the P3 region proteins of poliovirus. The P3 protein expressed from the recombinant vaccinia virus VV-P3 exhibited in vivo proteolytic %%%activity%%% as evident by processing of the polyprotein to generate the 3CD protein, consisting of a fusion between the 3C-pro and 3D-%%%pol%%% %%%proteins%%%. Further processing of the 3CD protein to 3C-pro and 3D-pol, however, was not detected in cells infected with VV-P3. Subcellular fractionation of VV-P3-infected cells demonstrated that the 3CD protein was present in both the soluble and membrane fractions. Finally, the 3CD protein expressed from VV-P3 was

stable in cells co-infected with VV-P3 and poliovirus and no further processing to 3D-pol was detected. These results are discussed with regards to in vivo studies which suggest that the 3CD polyprotein is not a precursor to 3D-pol in poliovirus-infected cells.

6/7/74 (Item 21 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0008649912 BIOSIS NO.: 199345080894
Cytotoxic T-lymphocyte (CTL) %%%activity%%% to HIV proteins and CD8 subpopulations in HIV positive children
BOOK TITLE: IXth International Conference on AIDS in affiliation with the IVth STD World Congress
AUTHOR: Aldhous M C (Reprint); Watret K C (Reprint); Froebel K S (Reprint); Mok J Y Q; Bird A G (Reprint)
BOOK AUTHOR/EDITOR: IXTH INTERNATIONAL CONFERENCE ON AIDS AND THE IVTH STD WORLD CONGRESS
AUTHOR ADDRESS: HIV Immunol. Unit, Royal Infirmary, Scotland, UK**UK
p217 1993
BOOK PUBLISHER: IXth International Conference on AIDS {a}, Berlin, Germany
CONFERENCE/MEETING: Meeting Berlin, Germany June 6-11, 1993; 19930606
DOCUMENT TYPE: Meeting
RECORD TYPE: Citation
LANGUAGE: English

6/7/75 (Item 22 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0006564412 BIOSIS NO.: 198987012303
ISOLATION AND CHARACTERIZATION OF SIMIAN IMMUNODEFICIENCY VIRUS FROM MANDRILLS IN AFRICA AND ITS RELATIONSHIP TO OTHER HUMAN AND SIMIAN IMMUNODEFICIENCY VIRUSES
AUTHOR: TSUJIMOTO H (Reprint); COOPER R W; KODAMA T; FUKASAWA M; MIURA T; OHTA Y; ISHIKAWA K-I; NAKAI M; FROST E; ET AL
AUTHOR ADDRESS: DEP ANIM PATHOL, INST MED SCI, UNIV TOKYO, MINATO-KU, TOKYO 108**JAPAN
JOURNAL: Journal of Virology 62 (11): p4044-4050 1988
ISSN: 0022-538X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Two isolates of simian retrovirus related to the human immunodeficiency virus (HIV) were obtained from apparently healthy mandrills, Papio (Mandrillus) sphinx, in western equatorial Africa. This virus, designated SIVMND (simian immunodeficiency virus from mandrills), appeared morphologically similar to HIV by electron microscopy, showed Mg2+-dependent reverse transcriptase %%%activity%%%, and induced cytopathic effect in human CD4-positive cells. Western blotting (immunoblotting) analyses revealed that the gag and pol products of SIVMND showed cross-reactivity with those of known HIVs and SIVs. Molecular clones covering full-length viral DNA were obtained from closed circular extrachromosomal DNA of SIVMND-infected cells. By clone-on-clone hybridization with known retroviruses of the HIV and SIV groups, SIVMND showed similar cross-hybridization with HIV-1, HIV-2, SIVAGM (African green monkey-derived SIV), and SIVMAC (rhesus macaque-derived SIV) in the gag and pol regions only at low stringency but not at high stringency, a result indicating that SIVMND is a new member of the HIV-SIV group. The existence of distinct SIVs in different monkey species suggest that recent interspecies transfer of HIV-SIV is unlikely in nature.

6/7/76 (Item 23 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0006214665 BIOSIS NO.: 198886054586

PROPERTIES OF AVIAN SARCOMA-LEUKOSIS VIRUS PP32-RELATED POL-ENDONUCLEASES PRODUCED IN ESCHERICHIA-COLI
AUTHOR: TERRY R (Reprint); SOLTIS D A; KATZMAN M; COBRINIK D; LEIS J; SKALKA A M
AUTHOR ADDRESS: FOX CHASE CANCER CENT, INST FOR CANCER RES, 7701 BURHOLME AVE, PHILADELPHIA, PA 19111, USA**USA
JOURNAL: Journal of Virology 62 (7): p2358-2365 1988
ISSN: 0022-538X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The gag-pol precursor protein of the avian sarcoma-leukosis virus is processed into three known pol-encoded mature polypeptides; the 95- and 63-kilodalton (kDa) .beta. and .alpha. subunits, respectively, of reverse transcriptase and the 32-kDa pp32 protein. The pp32 protein possesses DNA endonuclease %%%activity%%% and is produced from the precursor by two proteolytic cleavage events, one of which removes 4.1 kDa of protein from the C terminus. A 36-kDa protein (p36pol) which retains this C-terminal segment is detectable in small quantities in virions. We have conducted Escherichia coli plasmid clones that express the C-terminal domains of pol corresponding to pp32 and p36. These proteins have been purified by column chromatographic methods to near homogeneity. No significant differences could be detected in the enzymatic properties of the bacterially produced p21pol and p36pol proteins. Both possess DNA endonuclease %%%activity%%% and, like the pp32 protein isolated from virions, can cleave near the junction of two tandem avian sarcoma-leukosis virus long terminal repeats in double-stranded supercoiled DNA substrates. In the presence of Mg2+, both p32pol and viral p32 cleave either strand of DNA 2 nucleotides 5' to the junction.

? t s7/7/1-2

7/7/1 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0011121073 BIOSIS NO.: 199799755133
More reliable diagnosis of infection with human immunodeficiency virus type 1 (HIV-1) by detection of antibody IgGs to pol and gag proteins of HIV-1 and p24 antigen of HIV-1 in urine, saliva, and/or serum with highly sensitive and specific enzyme immunoassay (immune complex transfer enzyme immunoassay): A %%%review%%%
AUTHOR: Hashida Seiichi; Hashinaka Kazuya; Ishikawa Setsuko; Ishikawa Eiji (Reprint)
AUTHOR ADDRESS: Dep. Biochem., Miyazaki Med. College, Kiyotake, Miyazaki 889-16, Japan**Japan
JOURNAL: Journal of Clinical Laboratory Analysis 11 (5): p267-286 1997 1997
ISSN: 0887-8013
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Ultrasensitive enzyme immunoassays (immune complex transfer enzyme immunoassays) were developed for antibody IgGs to HIV-1 using recombinant reverse transcriptase (rRT), p17 (rp17), and p24 (rp24) as antigens. Antibody IgGs were reacted with 2, 4-dinitrophenyl-recombinant antigens and recombinant antigen-beta-D-galactosidase conjugates, and the immune complexes formed. comprising the three components, were trapped onto polystyrene beads coated with (anti-2,4-dinitrophenyl group) IgG. After washing, the immune complexes were eluted from the polystyrene beads with excess of epsilon-N2,4-dinitrophenyl-L-lysine and were transferred to clean polystyrene beads coated with (antihuman IgG gamma-chain) IgG. beta-D-Galactosidase %%%activity%%% bound to the last polystyrene beads was assayed by fluorometry. By transfer of the immune complexes from one solid phase to another, the nonspecific binding of the beta-D-galactosidase conjugates was minimized and the sensitivity was markedly improved. The immune complex transfer enzyme immunoassays using rRT, rp17, and rp24 as antigens were 300-1,000-fold, 1,000-3,000-fold,

and 30-100-fold, respectively, more sensitive than Western blotting for the corresponding antigens and 10-300-fold more sensitive than a conventional ELISA and a gelatin particle agglutination test. For urine (100 mu-l), whole saliva (1 mu-l), and serum (1 mu-l) samples, the sensitivity and specificity of the immune complex transfer enzyme immunoassay using rRT as antigen were both 100%. However, for urine samples in which the specific activities of antibody IgG to RT, p17, and p24 were much lower than those in serum samples probably due tb degradation by the kidney, a longer assay of bound beta-D-galactosidase %%%activity%%% or/and a concentration process for urine was required. The use of more than 1 mu-l of whole saliva was recommended for reliable diagnosis of the infections, whereas 1 mu-l of serum was sufficient for the purpose. The positivity with rRT as antigen could be confirmed by demonstration of antibody IgGs to p17 and p24 in most of the urine, whole saliva, and serum samples. In HIV-1 seroconversion serum panels, antibody IgG to p17 was detected as early as or even earlier than antibodies to HIV-1 by a conventional ELISA or/and a gelatin particle agglutination test, whereas antibody IgGs to RT and p24 were detected as early as or later than antibody IgG to p17. Thus the uses of rRT and rp17 as antigens were advantageous over that of the other antigens for randomly collected serum samples probably long after the infection and serum samples at early stages of the infection, respectively. On the basis of these results and other reports, the immune complex transfer enzyme immunoassay was developed for simultaneous detection of p24 antigen and antibody IgGs to RT and p17 in a single assay tube, and the window period (8 weeks, although widely variable), during which diagnosis of HIV-1 infection is not possible due to the absence of detectable antibodies to HIV-1, was shortened by 2 weeks. As a result, the simultaneous detection made possible not only as early diagnosis as that by detection of p24 antigen, but also as reliable diagnosis as that by detection of antibodies to HIV-1. Finally, the immune complex transfer enzyme immunoassay has been recently improved so as to be performed within shorter periods of time (2-3 hr) with higher sensitivity, and testing many samples has become easy.

7/7/2 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0009019696 BIOSIS NO.: 199497040981
Picornavirus nonstructural proteins: Emerging roles in virus replication and inhibition of host cell functions
AUTHOR: Porter Alan G
AUTHOR ADDRESS: Inst. Mol. Cell Biol., Natl. Univ. Singapore, 10 Kent Ridge Crescent, Singapore 0511, Singapore**Singapore
JOURNAL: Journal of Virology 67 (12): p6917-6921 1993 1993
ISSN: 0022-538X
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Citation
LANGUAGE: English

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ENV Reviews

10/7/1 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

19412482 PMID: 16107223
Retroviral superinfection resistance.
Nethe Micha; Berkhout Ben; van der Kuyl Antoinette C
Dept. of Human Retrovirology, Academic Medical Centre, University of Amsterdam, Meibergdreef 15, 1105AZ Amsterdam, The Netherlands. michanethe@hotmail.com
Retrovirology electronic resource (England) Aug 18 2005, 2 p52,
ISSN 1742-4690--Electronic Journal Code: 101216893
Publishing Model Electronic
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: In Process

The retroviral phenomenon of superinfection resistance (SIR) defines an interference mechanism that is established after primary infection, preventing the infected cell from being superinfected by a similar type of virus. This %%%review%%% describes our present understanding of the underlying mechanisms of SIR established by three characteristic retroviruses: Murine Leukaemia Virus (MuLV), Foamy Virus (FV), and Human Immunodeficiency Virus (HIV). In addition, SIR is discussed with respect to HIV superinfection of humans. MuLV resistant mice exhibit two genetic resistance traits related to SIR. The cellular Fv4 gene expresses an Env related protein that establishes resistance against MuLV infection. Another mouse gene (Fv1) mediates MuLV resistance by expression of a sequence that is distantly related to Gag and that blocks the viral infection after the reverse transcription step. FVs induce two distinct mechanisms of superinfection resistance. First, expression of the %%%Env%%% %%%protein%%% results in SIR, probably by occupancy of the cellular receptors for FV entry. Second, an increase in the concentration of the viral Bet (Between-env-and-LTR-1-and-2) protein reduces proviral FV gene expression by inhibition of the transcriptional activator protein Tas (Transactivator of spumaviruses). In contrast to SIR in FV and MuLV infection, the underlying mechanism of SIR in HIV-infected cells is poorly understood. CD4 receptor down-modulation, a major characteristic of HIV-infected cells, has been proposed to be the main mechanism of SIR against HIV, but data have been contradictory. Several recent studies report the occurrence of HIV superinfection in humans; an event associated with the generation of recombinant HIV strains and possibly with increased disease progression. The role of SIR in protecting patients from HIV superinfection has not been studied so far. The phenomenon of SIR may also be important in the protection of primates that are vaccinated with live attenuated simian immunodeficiency virus (SIV) against pathogenic SIV variants. As primate models of SIV infection closely resemble HIV infection, a better knowledge of SIR-induced mechanisms could contribute to the development of an HIV vaccine or other antiviral strategies.

Record Date Created: 20050922
Date of Electronic Publication: 20050818

10/7/2 (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

18683502 PMID: 16155609

Human T-cell leukemia/lymphoma virus type 1 nonstructural genes and their functions.

Nicot Christophe; Harrod Robert L; Ciminale Vincenzo; Franchini Genoveffa
Department of Microbiology, University of Kansas Medical Center, Molecular Genetics, and Immunology, 3025 Wahl Hall West, 3901 Rainbow Boulevard, Kansas City, KS 66160-7420, USA.

Oncogene (England) Sep 5 2005, 24 (39) p6026-34, ISSN 0950-9232
Journal Code: 8711562
Publishing Model Print
Document type: Journal Article; Review; Review, Tutorial
Languages: ENGLISH
Main Citation Owner: NLM
Record type: MEDLINE; Completed

The human T-cell leukemia/lymphoma virus (HTLV) genome, in addition to the structural Gag and %%%Env%%% %%%proteins%%% and retroviral enzymes, carries a region at its 3' end originally designated pX. To date, we know that this region encodes two essential transcriptional and post-transcriptional positive regulators of viral expression, the Tax and Rex proteins, respectively (reviewed elsewhere in this issue). Here, we will %%%review%%% current knowledge of the functions of three additional proteins encoded in the pX region, p12I, p13II, and p30II. (54 Refs.)

Record Date Created: 20050912
Record Date Completed: 20051004

10/7/3 (Item 3 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

17561233 PMID: 15578992

Strategies for retargeted gene delivery using vectors derived from lentiviruses.

Bartosch Birke; Cosset Francois-Loic

Laboratoire de Vectorologie Retrovirale et Therapie Genique, Unite de Virologie Humaine, INSERM U412, Ecole Normale Superieure de Lyon, 46 allee d'Italie. 69364 Lyon 07, France.

Current gene therapy (Netherlands) Dec 2004, 4 (4) p427-43, ISSN 1566-5232 Journal Code: 101125446

Publishing Model Print

Document type: Journal Article; Review

Languages: ENGLISH

Main Citation Owner: NLM

Record type: MEDLINE; Completed

With the development of the first viral vector systems 20 years ago [Mann et al., 1983; Watanabe and Temin, 1983] gene therapy strategies have come to the forefront of novel therapeutics [Cavazzana-Calvo et al., 2000]. A deeper understanding of vector biology and the molecular mechanisms of disease alongside tremendous advances in vector technology have significantly advanced the field of human gene therapy. Over the last few years several challenges needed to be overcome in order to bring gene therapy strategies closer to the clinic. These hurdles include the preparation of large amounts of stable, high titre vectors, minimising vector-related immunology and last but not least targeting infection and transgene expression to tissue or cells, which in many cases are not or only slowly dividing. Viral vectors are useful vehicles for the delivery of foreign genes into target cells, and retroviral vectors have been popular because of their ability to integrate into the host cell genome and maintain persistent gene expression. Moreover, lentiviruses, members of the retroviral family, have the ability to infect cells at both mitotic and post-mitotic stages of the cell cycle thus opening up the possibility to target non-dividing target cells and tissues. Human immunodeficiency virus (HIV) based vectors have been used in vitro and in vivo in a number of situations, however, safety concerns still exist, and therefore the development of vector systems based on primate as well as non-primate lentiviruses is ongoing. Concomitantly with lentiviral vector design, much has been learned about the incorporation of heterologous %%%env%%% %%%proteins%%% on lentiviral cores in order to combine specific targeting properties of envelope glycoproteins with the biological properties of lentiviral vectors. In this %%%review%%% article we will give an overview over advantages lentiviral vector systems offer. We will then discuss the current state of our understanding of the structure and function of viral envelope glycoproteins and emerging targeting strategies based on retroviral and lentiviral vector systems. (195 Refs.)

Record Date Created: 20041206

Record Date Completed: 20050331

10/7/4 (Item 4 from file: 155)

16414308 PMID: 15279588

Glycosylation of the ENV spike of primate immunodeficiency viruses and antibody neutralization.

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Department of Infectious Diseases, Children's Hospital, Boston, MA 02115, USA. cherylpikora@childrens.harvard.edu

Current HIV research (Netherlands) Jul 2004, 2 (3) p243-54, ISSN 1570-162X Journal Code: 101156990

Publishing Model Print

Document type: Journal Article; Review; Review, Tutorial

Languages: ENGLISH

Main Citation Owner: NLM

Record type: MEDLINE; Completed

Neutralizing antibody titers have been correlated with protection following vaccination against many viral pathogens. The logical target of protective antibody responses elicited by potential HIV vaccines should be the viral Env spike on the surface of the virion. However, the potency and titers of neutralizing antibodies that arise during HIV infection are generally discouragingly low and the antibodies that do arise recognize mainly autologous virus. This is thought to be a result of a combination of

immunodominance of hypervariable regions of the %%%Env%%% %%%protein%%% that can easily escape neutralization, antibody reactivity to gp160 "decoy" protein in cell surface debris or monomeric gp120, conformational constraints within the Env trimer that create unfavorable antibody binding conditions and extensive glycosylation of the exposed regions of Env within the trimer. This %%%review%%% will describe current knowledge regarding glycosylation as a mechanism of neutralization resistance and discuss experimental approaches used to overcome this resistance. Part of the strategy toward development of an optimally immunogenic Env spike will likely require modification of Env glycosylation. Copyright 2004 Bentham Science Publishers Ltd. (121 Refs.)
Record Date Created: 20040728
Record Date Completed: 20050105

10/7/5 (Item 5 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

14917203 PMID: 12908770
The foamy virus envelope glycoproteins.
Lindemann D; Goepfert P A
Institut fur Virologie, Medizinische Fakultat Carl-Gustav-Carus, Technische Universitat Dresden, Fetscherstrasse 74, 01307 Dresden, Germany. dirk.lindemann@mailbox.tu-dresden.de
Current topics in microbiology and immunology (Germany) 2003, 277 p111-29, ISSN 0070-217X Journal Code: 0110513
Contract/Grant No.: K08-AI-01380; AI; NIAID
Publishing Model Print
Document type: Journal Article; Review; Review, Tutorial
Languages: ENGLISH
Main Citation Owner: NLM
Record type: MEDLINE; Completed
The main functions of retroviral glycoproteins are recognition and binding to the cellular virus receptor as well as fusion of viral and cellular lipid membranes to release the viral particle into the cytoplasm of the host cell. Foamy viruses (FVs) are a special group of retroviruses with a very broad host range that use a currently unknown cellular receptor for entry. Nevertheless, many functions of the FV envelope glycoproteins in the viral replication cycle have been characterized in detail over the last years. Several unique features not found for any other retrovirus were identified. These include the presence of two types of FV %%%Env%%% %%%proteins%%% , gp170(Env-Bet) and gp130Env, and the strict requirement of gp130Env coexpression for the FV budding and particle release process, a function that cannot be compensated for by any other viral glycoprotein tested so far. Furthermore, domains in gp130Env could be characterized that influence its intracellular distribution, cell surface transport, and its specific interaction with the viral capsid during particle egress. In addition, it has recently been shown that gp130Env expression alone induces release of subviral particles from cells. This %%%review%%% summarizes the current knowledge about the nature of the FV %%%Env%%% %%%proteins%%% and their function in the viral replication cycle. (41 Refs.)
Record Date Created: 20030811
Record Date Completed: 20030910

10/7/6 (Item 6 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

13200669 PMID: 11249668
Retroviral cell targeting vectors.
Buchholz C J; Stitz J; Cichutek K
Medizinische Biotechnologie, Paul-Ehrlich-Institut, Paul-Ehrlich-Strasse 51-59, 63225 Langen, Germany. bucch@pei.de
Current opinion in molecular therapeutics (England) Oct 1999, 1 (5) p613-21, ISSN 1464-8431 Journal Code: 100891485
Publishing Model Print
Document type: Journal Article; Review; Review, Tutorial
Languages: ENGLISH
Main Citation Owner: NLM

Record type: MEDLINE; Completed

The availability of cell targeting vectors is an unalterable requirement for in vivo gene therapy trials. This %%%review%%% will describe the different strategies developed over the past few years in order to target retroviral vectors to preselected human cell types by genetic modification of the envelope (%%%Env%%%) %%%proteins%%% . Current targeting concepts include the substitution of the complete %%%Env%%% %%%protein%%% as well as the incorporation of new receptor binding domains into the %%%Env%%% %%%protein%%% . These approaches are aimed at altering the host range of vectors with a natural tropism for non-human cells to specific human cell types, or achieving tissue-specificity for vectors that would naturally infect a wide spectrum of human cell types. Targeting concepts and efficient targeting vectors with potential for clinical trials will be described, and their advantages and disadvantages will be discussed. (58 Refs.)

Record Date Created: 20010315

Record Date Completed: 20010412

10/7/7 (Item 7 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

12993786 PMID: 10952216

Cell-surface area codes: mobile-element related gene switches generate precise and heritable cell-surface displays of address molecules that are used for constructing embryos.

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Genetica (NETHERLANDS) 1999, 107 (1-3) p249-59, ISSN 0016-6707 Journal Code: 0370740

Publishing Model Print

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: MEDLINE; Completed

We present an updated area code hypothesis supporting the proposal that cell surface display of seven-transmembrane olfactory receptors, protocadherins and other cell surface receptors provide codes that enable cells to find their correct partners as they sculpture embryos. The genetic mechanisms that program the expression of such displays have been largely unknown until very recently. However, increasing evidence now suggests that precise developmental control of the expression of these genes during embryogenesis is achieved in part by permanent and heritable changes in DNA. Using the developing immune system as a model, we discuss two different types of developmentally programmed genetic switches, each of which relies on recombination mechanisms related to mobile elements. We %%%review%%% new evidence suggesting the involvement of mobile element related switch mechanisms in the generation of protocadherin molecules, and their possible involvement in the control of expressions of olfactory receptors. As both recombinase and reverse transcriptase mechanisms play a role in the switching of the immunoglobulin genes, we searched the databases of expressed sequence tags (dbEST) for expression of related genes in other tissues. We present data revealing that transposases and reverse transcriptases are widely expressed in most tissues. We also searched these databases for expression of env (envelope) gene products, stimulated by provocative results suggesting that these molecules might function as cellular address receptors. We found that env genes are also expressed in large numbers in normal human tissues. One must assume that these three different types of mobile-element-related messenger RNA molecules (transposases, reverse transcriptases, and %%%env%%% %%%proteins%%%) are expressed for use in functions of value in the various tissues and have been preserved in the genome because of their selective advantages. We conclude that it is possible that many specific cell lineage decisions are made and remembered by means of genetic switches similar to those that control the immunoglobulin and protocadherin and, probably, the seven transmembrane/olfactory gene families. We also conclude that complex genetic programs utilizing mobile-element-related genes program these events.

Record Date Created: 20000907

Record Date Completed: 20000907

10/7/8 (Item 8 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

11617652 PMID: 8930674
The potential roles of endogenous retroviruses in autoimmunity.
Nakagawa K; Harrison L C
Burnet Clinical Research Unit, Walter and Eliza Hall Institute of Medical Research, Royal Melbourne Hospital, Parkville, Australia.
Immunological reviews (DENMARK) Aug 1996, 152 p193-236, ISSN 0105-2896 Journal Code: 7702118
Publishing Model Print
Document type: Journal Article; Review
Languages: ENGLISH
Main Citation Owner: NLM
Record type: MEDLINE; Completed

Endogenous retroviruses (ERVs) are estimated to comprise up to 1% of human DNA. While the genome of many ERVs is interrupted by termination codons, deletions or frame shift mutations, some ERVs are transcriptionally active and recent studies reveal protein expression or particle formation by human ERVs. ERVs have been implicated as aetiological agents of autoimmune disease, because of their structural and sequence similarities to exogenous retroviruses associated with immune dysregulation and their tissue-specific or differentiation-dependent expression. In fact, retrovirus-like particles distinct from those of known exogenous retroviruses and immune responses to ERV proteins have been observed in autoimmune disease. Quantitatively or structurally aberrant expression of normally cryptic ERVs, induced by environmental or endogenous factors, could initiate autoimmunity through direct or indirect mechanisms. ERVs may lead to immune dysregulation as insertional mutagens or cis-regulatory elements of cellular genes involved in immune function. ERVs may also encode elements like tax in human T-lymphotrophic virus type I (HTLV-I) or tat in human immunodeficiency virus-I (HIV-I) that are capable of transactivating cellular genes. More directly, human ERV gene products themselves may be immunologically active, by analogy with the superantigen activity in the long terminal repeat (LTR) of mouse mammary tumour viruses (MMTV) and the non-specific immunosuppressive activity in mammalian type C retrovirus %%%env%%% %%%protein%%%. Alternatively, increased expression of an ERV protein, or expression of a novel ERV protein not expressed in the thymus during acquisition of immune tolerance, may lead to its perception as a neoantigen. Paraneoplastic syndromes raise the possibility that novel ERV-encoded epitopes expressed by a tumour elicit immunity to cross-reactive epitopes in normal tissues. Recombination events between different but related ERVs, to whose products the host is immunologically tolerant, may also generate new antigenic determinants. Frequently reported humoral immunity to exogenous retrovirus proteins in autoimmune disease could be elicited by cross-reactive ERV proteins. A %%%review%%% of the evidence implicating ERVs in immune dysfunction leads to the conclusion that direct molecular studies are likely to establish a pathogenic role for ERVs in autoimmune disease. (219 Refs.)

Record Date Created: 19970221
Record Date Completed: 19970221

10/7/9 (Item 9 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07522141 PMID: 3008001
Expression of the HTLV-III envelope gene by a recombinant vaccinia virus.
Chakrabarti S; Robert-Guroff M; Wong-Staal F; Gallo R C; Moss B
Nature (ENGLAND) Apr 10-16 1986, 320 (6062) p535-7, ISSN 0028-0836 Journal Code: 0410462
Publishing Model Print
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: MEDLINE; Completed

The discovery that the aetiological agent of acquired immune deficiency syndrome (AIDS) is a retrovirus, referred to as human T-lymphotropic virus type III (HTLV-III) or lymphadenopathy-associated virus (LAV) (for %%%review%%% see ref. 1), has raised the possibility of developing a vaccine. In this regard, the envelope (%%%env%%%) %%%proteins%%% of murine retroviruses can induce protective immunity in mice. The HTLV-III env gene specifies a primary polypeptide of approximately 860 amino acids that is glycosylated to form a precursor of relative molecular mass (Mr) 160,000 (gp160), which gives rise to mature membrane-associated proteins of Mr 120,000 (gp120) and 41,000 (gp41). The HTLV-III env gene has been expressed in Escherichia coli and by simian virus 40 (SV40) vectors but formation of the authentic proteins has not been demonstrated. Here, we describe the expression of the complete env gene by a vaccinia virus vector. Evidence is presented that synthesis, glycosylation, processing and membrane transport of the env polypeptide occurred without other HTLV-III gene functions; the %%%env%%% %%%protein%%% was recognized by sera from unrelated AIDs patients; and a single vaccination with the infectious recombinant vaccinia virus induced antibodies to gp120 in mice.
Record Date Created: 19860522
Record Date Completed: 19860522

10/7/10 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0015184043 BIOSIS NO.: 200500091108
Untitled
AUTHOR: Mansour Tarek S; Sum Phaik-Eng
JOURNAL: Current Medicinal Chemistry - Anti-Infective Agents 4 (1): p1 January 2005 2005
MEDIUM: print
ISSN: 1568-0126 _(ISSN print)
DOCUMENT TYPE: Article; Literature Review; Editorial
RECORD TYPE: Citation
LANGUAGE: English

10/7/11 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0014377280 BIOSIS NO.: 200300345999
HIV-1 replication and pathogenesis in the human thymus.
AUTHOR: Meissner Eric G; Duus Karen M; Loomis Rebecca; D'Agostin Rhiannon; Su Lishan (Reprint)
AUTHOR ADDRESS: Lineberger Comprehensive Cancer Center, Department of Microbiology and Immunology, School of Medicine, University of North Carolina, Chapel Hill, NC, 27599-7295, USA**USA
AUTHOR E-MAIL ADDRESS: lsu@med.unc.edu
JOURNAL: Current HIV Research 1 (3): p275-285 July 2003 2003
MEDIUM: print
ISSN: 1570-162X _(ISSN print)
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Citation
LANGUAGE: English

10/7/12 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0013904292 BIOSIS NO.: 200200497803
Assembling the human immunodeficiency virus type 1
AUTHOR: Cimarelli A; Darlix J-L (Reprint)
AUTHOR ADDRESS: Laboretro, U412, Ecole Normale Superieure de Lyon, 46 Allee d'Italie, 69364, Lyon, France**France
JOURNAL: CMLS Cellular and Molecular Life Sciences 59 (7): p1166-1184 July, 2002 2002
MEDIUM: print
ISSN: 1420-682X

DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Retroviral assembly proceeds through a series of concerted events that lead to the formation and release of infectious virion particles from the infected cell. Upon translation, structural proteins are targeted to the plasma membrane where they accumulate. There, the nascent particle forces the plasma membrane to form a bud, which pinches off releasing the virion particle from the cell. In this %%%review%%% we describe the molecular mechanisms now known to be behind the process of virion assembly. In particular, we focus on the human immunodeficiency virus type 1, the prototype member of the lentivirus subfamily of the Retroviridae.

10/7/13 (Item 4 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0011905689 BIOSIS NO.: 199900165349
Foamy viruses are unconventional retroviruses
AUTHOR: Linial Maxine L (Reprint)
AUTHOR ADDRESS: Div. Basic Sci., Fred Hutchinson Cancer Res. Cent., 1100 Fairview Ave. N., Seattle, WA 98109, USA**USA
JOURNAL: Journal of Virology 73 (3): p1747-1755 March, 1999 1999
MEDIUM: print
ISSN: 0022-538X
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Citation
LANGUAGE: English

10/7/14 (Item 5 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0011478954 BIOSIS NO.: 199800273201
Avian leukosis virus-receptor interactions
AUTHOR: Young John A T (Reprint)
AUTHOR ADDRESS: Dep. Microbiol. Mol. Genet., Harvard Med. Sch., 200 Longwood Ave., Boston, MA 02115, USA**USA
JOURNAL: Avian Pathology 27 (SUPPL. 1): pS21-S25 April, 1998 1998
MEDIUM: print
ISSN: 0307-9457
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Cellular receptors for subgroups A, B, D and E avian leukosis virus (ALV) have been identified and characterized. The Tva receptor for subgroup A ALV is a member of the low density lipoprotein receptor family of proteins. There is an accumulating body of evidence to suggest that this receptor binds specifically to subgroup A viral envelope (%%%Env%%% %%%proteins%%% and induces conformational changes in %%%Env%%% %%%proteins%%% that are similar to those expected of the fusion active form of the viral glycoprotein. In contrast to the Tva receptor, Tvb receptors for viral subgroups B, D, and E are members of the tumour necrosis factor receptor (TNFR) protein family. Like several other members of this protein family, the Tvb proteins possess a cytoplasmic death domain and have been shown to induce cell death following binding to a soluble subgroup B Env-specific reagent. These studies suggest a model in which the interactions between subgroup B and D %%%Env%%% %%%proteins%%% and their Tvb receptors contribute to the cytopathic effects that are associated with infection of cells by ALV-B and ALV-D.

10/7/15 (Item 6 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0010930910 BIOSIS NO.: 199799564970
A role for rev in the association of HIV-1 gag mRNA with cytoskeletal beta-actin and viral protein expression
AUTHOR: Kimura T; Hashimoto I; Nishikawa M; Fujisawa J I
AUTHOR ADDRESS: Dep. Microbiol., Kansai Med. Univ., Moriguchi, Osaka 570, Japan**Japan
JOURNAL: Biochimie (Paris) 78 (11-12): p1075-1080 1996 (1997) 1996
ISSN: 0300-9084
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Human immunodeficiency virus type-1 (HIV-1) Rev acts by inducing the specific nucleocytoplasmic transport of a class of incompletely spliced RNAs that encodes the viral structural proteins. The transfection of HeLa cells with a rev-defective HIV-1 expression plasmid, however, resulted in the export of overexpressed, intron-containing species of viral RNAs, possibly through a default process of nuclear retention. Thus, this system enabled us to directly compare Rev+ and Rev- cells as to the usage of RRE-containing mRNAs by the cellular translational machinery. Biochemical examination of the transfected cells revealed that although significant levels of gag and env mRNAs were detected in both the presence and absence of Rev, efficient production of viral proteins was strictly dependent on the presence of Rev. A fluorescence in situ hybridisation assay confirmed these findings and provided further evidence that even in the presence of Rev, not all of the viral mRNA was equally translated. At the early phase of RNA export in Rev+ cells, gag mRNA was observed throughout both the cytoplasm and nucleoplasm as uniform fine stippling. In addition, the mRNA formed clusters mainly in the perinuclear region, which were not observed in Rev- cells. In the presence of Rev, expression of the gag protein was limited to these perinuclear sites where the mRNA accumulated. Subsequent staining of the cytoskeletal proteins demonstrated that in Rev+ cells gag mRNA is colocalized with beta-actin in the sites where the RNA formed clusters. In the absence of Rev, in contrast, the gag mRNA failed to associate with the cytoskeletal proteins. These results suggest that in addition to promoting the emergence of intron-containing RNA from the nucleus, Rev plays an important role in the compartmentation of translation by directing RRE-containing mRNAs to the beta-actin to form the perinuclear clusters at which the synthesis of viral structural proteins begins.

10/7/16 (Item 7 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0010552649 BIOSIS NO.: 199699186709
Role of apoptosis in the pathogenesis of human virus disease
AUTHOR: Wattre P (Reprint); Bert V; Hober D
AUTHOR ADDRESS: Lab. de virol., batiment IRFPPS, CHRU, 59037 Lille Cedex, France**France
JOURNAL: Annales de Biologie Clinique 54 (5): p189-197 1996 1996
ISSN: 0003-3898
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: French

ABSTRACT: Homeostasis of cell numbers in tissues is maintained by a critical balance between cell proliferation and programmed cell death or apoptosis. Many human viruses are able to develop suitable strategies for modifying apoptosis in virus-infected cells and in virus-primed T cells. Apoptosis is characterized by the fragmentation of nuclear DNA into 180-200 bp apoptotic bodies and can be analysed microscopically or by flow cytometry using staining with various dyes. Moreover DNA cleavage can be identified by electrophoresis and by specific labeling using in situ nucleotidytransferase assay (ISNT), terminal deoxynucleotidyltransferase-mediated dUTP nick-end labeling technique (Tunel), or by Elisa. Adenovirus E1A induces expression of protooncogenes c-myc and c-fos which sensitize cells to apoptosis; EBV EBNA-5, and adenovirus E1A, HPV E7, and polyomavirus large T act in the same way by displacing pRB-bound E2F. EBV EBNA-5, HPV E6, Adenovirus E1B 55 kDa

inactivate the tumor suppressor protein p53 and engage the cells in the transformation process. EBV LMP-1, HHV6, and HTLV1 tax induce the antiapoptotic bcl-2 protein. EBV BHRF1 encodes proteins with homology to bcl-2 and Adenovirus E1B 19 kDa encodes proteins that have protective functions similar to bcl-2. Activated lymphocytes responding to viral infections express high levels of fas and are susceptible to apoptosis. TNF-alpha can down- or up-regulate fas and down-regulates TNF-R. Adenovirus E1B 19 kDa blocks the proapoptotic activity of TNF-alpha. Inversely, Cytomegalovirus, hepatitis C virus and Myxoviruses up-regulate fas antigen prior to undergoing apoptosis. In HIV-infected patients, CD4+ T-cell apoptosis is mediated by the cytopathic effect of the virus and the cell surface expression of gp 120-%%%env%%% %%%protein%%%. Moreover, on accelerated T-cell apoptosis in HIV-infected individuals is characterized by (i) HIV gp120-CD4+ cross-linking and subsequent aberrant signaling of T-cells, (ii) involvement of TNF alpha-fas/Apo-1 (TNF-R) binding, (iii) involvement of accessory cells as an apoptosis inducer and as a result of defective antigen presentation, (iv) possible superantigen activity induced by HIV products and cofactors. Many viruses also encode proteins with protease activity which could induce apoptosis. The induction of apoptosis may result in virus cell clearance, in contrast the inhibition of apoptosis may result in virus cell transformation and viral persistence. Indirectly, the apoptosis of infected cells may be induced by CTs, NK cells and cytokines. In addition, apoptosis-mediated physiological depletion of T lymphocytes in the course of viral infection can silence the immune response and can induce immunodeficiency.

10/7/17 (Item 8 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0010134797 BIOSIS NO.: 199698602630
Proteins of bovine leukemia virus and human T-cell leukemia viruses
AUTHOR: Hruskova-Heidingsfeldova O
AUTHOR ADDRESS: Dep. Biochem., Inst. Organic Chem. Biochem., Acad. Sci. Czech Republic, 166 10, Praha 6, Czech Republic**Czech Republic
JOURNAL: Folia Biologica (Prague) 41 (5): p201-212 1995 1995
ISSN: 0015-5500
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Citation
LANGUAGE: English

10/7/18 (Item 9 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0008449987 BIOSIS NO.: 199344012882
HLA class I binding regions of HIV-1 proteins
AUTHOR: Choppin Jeannine; Guillet Jean-Gerard; Levy Jean-Paul
AUTHOR ADDRESS: Inst. Cochin Genetique Moleculaire, INSERM U. 152, 27 rue du Faubourg Saint-Jacques, 75014 Paris, France**France
JOURNAL: Critical Reviews in Immunology 12 (1-2): p1-16 1992
ISSN: 1040-8401
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Citation
LANGUAGE: English
? t s11/7/155-166

11/7/155 (Item 16 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0011433026 BIOSIS NO.: 199800227273
Diversity of HIV-1 Vpr interactions involves usage of the WXXF motif of host cell proteins
AUTHOR: Bouhamdan Mohamad; Xue Yanning; Baudat Yves; Hu Baocheng; Sire Josephine; Pomerantz Roger J; Duan Ling-Xun (Reprint)
AUTHOR ADDRESS: Dorrance H. Hamilton Lab., Cent. Hum. Virol., Div. Infectious Dis., Dep. Med., Jefferson Med. Coll., Thomas Jefferson Univ., Philadelphia, PA 19107, USA**USA

JOURNAL: Journal of Biological Chemistry 273 (14): p8009-8016 April 3, 1998 1998
MEDIUM: print
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Targeting protein or RNA moieties to specific cellular compartments may enhance their desired functions and specificities. Human immunodeficiency virus type I (HIV-1) encodes proteins in addition to Gag, Pol, and Env that are packaged into virus particles. One such retroviral-incorporated protein is Vpr, which is present in all primate lentiviruses. Vpr has been implicated in different roles within the HIV-1 life cycle. In testing a new hypothesis in which viral proteins are utilized as docking sites to incorporate protein moieties into virions, we used the peptide phage display approach to search for Vpr-specific binding peptides. In the present studies, we demonstrate that most of the peptides that bind to Vpr have a common motif, WXXF. More importantly, we demonstrate that the WXXF motif of uracil DNA glycosylase is implicated in the interaction of uracil DNA glycosylase with Vpr intracellularly. Finally, a dimer of the WXXF motif was fused to the chloramphenicol acetyl transferase (CAT) gene, and it was demonstrated that the WXXF dimer-CAT fusion protein construct produces CAT %%%activity%%% within virions in the presence of Vpr as a docking protein. This study provides a novel potential strategy in the targeting of antiviral agents to interfere with HIV-1 replication.

0011304198 BIOSIS NO.: 199800098445
DNA immunization of mice against SIVmac239 Gag and Env using Rev-independent expression plasmids
AUTHOR: Indraccolo Stefano; Feroli Fiorella; Minuzzo Sonia; Mion Marta; Rosato Antonio; Zamarchi Rita; Titti Fausto; Verani Paola; Amadori Alberto (Reprint); Chieco-Bianchi Luigi
AUTHOR ADDRESS: Dep. Oncol. Surgical Sci., via Gattamelata 64, 35128 Padua, Italy**Italy
JOURNAL: AIDS Research and Human Retroviruses 14 (1): p83-90 Jan. 1, 1998 1998
MEDIUM: print
ISSN: 0889-2229
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Simian immunodeficiency virus (SIV) structural gene expression, including gag and env, strictly depends on the interaction of the viral posttranscriptional regulator Rev with its target RNA, the Rev-responsive element (RRE). A small RNA element, termed the constitutive transport element (CTE), located in the 3' portion of simian retrovirus 1 (SRV-1) mRNA, can efficiently substitute for the human immunodeficiency virus (HIV) Rev-RRE interaction, and thus render HIV expression and replication Rev independent. We tested the ability of the SRV-1 CTE to drive the expression of SIVmac239 env and gag from subgenomic constructs designed for possible use in vaccine trials. In vivo expression studies showed that when the SRV-1 sequence is coupled to the SIV gag and env mRNAs, it functions in an orientation-dependent fashion, and leads to strong expression of SIV Gag and Env in human and monkey cell lines; levels of CTE-mediated protein expression were similar to those obtained with a functional Rev-RRE system. On the other hand, in murine fibroblast-like cells, SIV Gag and Env were expressed from constructs at relatively high levels even in the absence of Rev-RRE; nevertheless, their expression was increased by the presence of the SRV-1 CTE. As reported previously for HIV, the murine cell lines appeared to be defective for Rev-RRE %%%activity%%%, and required overexpression of Rev to induce a Rev response. Intramuscular injection of the gag-CTE and env-CTE constructs in BALB/c mice resulted in the expression of the corresponding mRNAs, and

the production of anti-Gag and anti-Env antibodies, thus suggesting that these vectors might be used for genetic immunization approaches.

11/7/157 (Item 18 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0010621676 BIOSIS NO.: 199699255736
Properties of virus-like particles produced by SIV-chronically infected human cell clones
AUTHOR: Kraiselburd Edmundo N (Reprint); Torres Jose V
AUTHOR ADDRESS: Dep. Microbiol. Med. Zool., UPR Sch. Med., Room B-315, P.O. Box 365067, San Juan, PR 00936-5067, Puerto Rico**Puerto Rico
JOURNAL: Cellular and Molecular Biology (Noisy-Le-Grand) 41 (SUPPL. 1): p S41-S52 1995 1995
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: SIV-sm chronically infected cultures were obtained after infection of CEMX174 cells with either SIV-smH3 or SIV-smE660. These phenotypicaly CD4+ cells, formed syncytia but only when cocultivated with CD4+ cells. Single cell clones were derived from these cultures and examined for the production of virus-specific proteins. The majority of the clones expressed SIV p27 antigen and low levels of virus reverse transcriptase %%%activity%%%. Western blot analysis, performed with either monoclonal or polyclonal sera, showed that a chronically infected clone (B7) produced particles which contained envelope (gp1135 and gp43), gag precursors and gag proteins (p27, p16 and p8). However, these particles (SIV-smB7) lacked detectable levels of vpx and of integrase, and contained several fusion proteins which expressed viral protease antigens. This defective virus failed to infect established CD4+ cell lines, as well as primary cultures of macrophages and of peripheral blood lymphocytes, obtained both from humans and from rhesus macaques. Lack of infection correlated with lack of viral DNA detection by PCR amplification of genomic DNA extracted from these cell cultures. In addition, SIV-smB7 virus lacked infectivity in vivo. Rhesus macaques inoculated with high concentrations of SIV-smB7 showed no viremia and their PBMC were PCR negative. Thus, B7 cells produced stable, non-infectious virus mutants, which contained env and gag proteins, but lacked detectable amounts of vpx and of enzymes required for virus replication. Due to the high constitutive expression of this virus-like particle, we are now testing this preparation as a vaccine.

11/7/158 (Item 19 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0010552649 BIOSIS NO.: 199699186709
Role of apoptosis in the pathogenesis of human virus disease
AUTHOR: Wattre P (Reprint); Bert V; Hober D
AUTHOR ADDRESS: Lab. de virol., batiment IRFPPS, CHRU, 59037 Lille Cedex, France**France
JOURNAL: Annales de Biologie Clinique 54 (5): p189-197 1996 1996
ISSN: 0003-3898
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: French

ABSTRACT: Homeostasis of cell numbers in tissues is maintained by a critical balance between cell proliferation and programmed cell death or apoptosis. Many human viruses are able to develop suitable strategies for modifying apoptosis in virus-infected cells and in virus-primed T cells. Apoptosis is characterized by the fragmentation of nuclear DNA into 180-200 bp apoptotic bodies and can be analysed microscopically or by flow cytometry using staining with various dyes. Moreover DNA cleavage can be identified by electrophoresis and by specific labeling using in situ nucleotidytransferase assay (ISNT), terminal deoxynucleotidyltransferase-mediated dUTP nick-end labeling technique

(Tunel), or by Elisa. Adenovirus E1A induces expression of protooncogenes c-myc and c-fos which sensitize cells to apoptosis; EBV EBNA-5, and adenovirus E1A, HPV E7, and polyomavirus large T act in the same way by displacing pRB-bound E2F. EBV EBNA-5, HPV E6, Adenovirus E1B 55 kDa inactivate the tumor suppressor protein p53 and engage the cells in the transformation process. EBV LMP-1, HHV6, and HTLV1 tax induce the antiapoptotic bcl-2 protein. EBV BHRF1 encodes proteins with homology to bcl-2 and Adenovirus E1B 19 kDa encodes proteins that have protective functions similar to bcl-2. Activated lymphocytes responding to viral infections express high levels of fas and are susceptible to apoptosis. TNF-alpha can down- or up-regulate fas and down-regulates TNF-R. Adenovirus E1B 19 kDa blocks the proapoptotic %%%activity%%% of TNF-alpha. Inversely, Cytomegalovirus, hepatitis C virus and Myxoviruses up-regulate fas antigen prior to undergoing apoptosis. In HIV-infected patients, CD4+ T-cell apoptosis is mediated by the cytopathic effect of the virus and the cell surface expression of gp 120-%%%env%%% %%%protein%%%. Moreover, on accelerated T-cell apoptosis in HIV-infected individuals is characterized by (i) HIV gp120-CD4+ cross-linking and subsequent aberrant signaling of T-cells, (ii) involvement of TNF alpha-fas/Apo-1 (TNF-R) binding, (iii) involvement of accessory cells as an apoptosis inducer and as a result of defective antigen presentation, (iv) possible superantigen %%%activity%%% induced by HIV products and cofactors. Many viruses also encode proteins with protease %%%activity%%% which could induce apoptosis. The induction of apoptosis may result in virus cell clearance, in contrast the inhibition of apoptosis may result in virus cell transformation and viral persistence. Indirectly, the apoptosis of infected cells may be induced by CTs, NK cells and cytokines. In addition, apoptosis-mediated physiological depletion of T lymphocytes in the course of viral infection can silence the immune response and can induce immunodeficiency.

11/7/159 (Item 20 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0010228112 BIOSIS NO.: 199698695945
A CD4 pentapeptide as an in vitro target for specific CTLs in HIV-1-infected individuals
AUTHOR: Achour Ammar (Reprint); Bizzini Bernard; Burny Arsene; Zagury Daniel; Zagury Jean-Francois
AUTHOR ADDRESS: Univ. Pierre et Marie Curie, 4 Place Jussieu, B.P. 198, 75252 Paris Cedex 05, France**France
JOURNAL: Immunology and Infectious Diseases (Oxford) 5 (4): p270-276 1995
1995
ISSN: 0959-4957
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: We have previously identified a pentapeptide (SLWDQ) common both to the CD4 molecule and HIV-1 gp120. This pentapeptide, highly conserved in all HIV-1 strains, is located within the T2 peptide known to be a helper and CTL T cell epitope (HEDIISLWDQSLK) on the %%%env%%% %%%protein%%% of human immunodeficiency virus type 1. Cell cultures were obtained by polyclonal activation using autologous blast cells and CTL lines generated from frozen peripheral blood lymphocytes of HIV-1 seropositive donors by stimulation with the T2 peptide and recombinant interleukin-2. We mapped the fine specificity of these CTLs directed towards the T2 sequence using short nested peptides, and found that the CD4 SLWDQ pentapeptide was the minimal epitope in this sequence. Furthermore the CTL %%%activity%%% directed towards this pentapeptide was restricted to HLA-A2 and HLA-A11 molecules. The presentation by MHC class I molecules of self short peptidic sequences is in line with a recently reported induction of cellular autoimmunity found associated to minimum peptidic residue requirements. Vaccine strategies based on gp120 antigen should take into account such a mechanism.

11/7/160 (Item 21 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0009605327 BIOSIS NO.: 199598073160
Systematic identification of H-2K-d binding peptides and induction of peptide specific CTL
AUTHOR: Gill Randall F; Abastado Jean-Pierre; Wei Wei-Zen (Reprint)
AUTHOR ADDRESS: Dep. Immunology, Breast Cancer Program, Mich. Cancer Foundation, 110 E. Warren Avenue, Detroit, MI 48201, USA**USA
JOURNAL: Journal of Immunological Methods 176 (2): p245-253 1994 1994
ISSN: 0022-1759
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Most peptides with putative MHC I restricted sequence motifs do not bind to the corresponding MHC I nor induce cytolytic T cells. There exist additional constraints which limit peptide binding and immunogenicity. To identify immunogenic peptides in novel protein sequences, it will be necessary to first evaluate peptide binding to MHC I. In this study, a soluble single chain fusion protein SC-K-d was used to evaluate potential K-d binding peptides from the sequences of mouse mammary tumor virus gag and %%%env%%% %%%proteins%%%. A total of 27 peptides were identified which displayed the reported K-d restricted motif. Of the 27 peptides, six demonstrated strong to moderate binding to SC-K-d. The strongest binding peptides expressed tyrosine or phenylalanine at position 2 and leucine at the C-terminus. The capability of MMTV peptides to induce CTL corresponds to their SC-K-d binding %%%activity%%%. Of the six peptides that demonstrated moderate to strong binding, five induced CTL in BALB/c mice. These peptides induced CTL after 1-3 in vivo immunizations followed by 5 day in vitro stimulation. Furthermore, a single in vitro stimulation of naive lymphocytes with strong-binding G425 was sufficient to induce significant CTL %%%activity%%%. Weak or non-binding peptides did not induce CTL. Therefore, peptide binding to SC-K-d is a predictive indicator of CTL inducing %%%activity%%%.

11/7/161 (Item 22 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0009429584 BIOSIS NO.: 199497450869
Induction of antigen-specific killer T lymphocyte responses using subunit SIV-mac251 gag and env vaccines containing QS-21 saponin adjuvant
AUTHOR: Newman Mark J (Reprint); Munrow Kenneth J; Anderson Christine A; Murphy Cheryl I; Panicali Dennis L; Seals Jonathan R; Wu Jia-Yan; Wyand Michael S; Kensil Charlotte R
AUTHOR ADDRESS: Apollon, Inc., 1 Great Valley Parkway, Malvern, PA 19355-1423, USA**USA
JOURNAL: AIDS Research and Human Retroviruses 10 (7): p853-861 1994 1994
ISSN: 0889-2229
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Subunit vaccines based on recombinant proteins have proved useful for inducing antibody responses and they are safe for widespread use because they do not contain any live components. Unfortunately, they do not typically induce the types of cell-mediated immune responses required to control viral pathogens; specifically, they do not induce CD8+ cytotoxic T lymphocyte (CTL) responses. To increase the immunogenicity of recombinant proteins, we have used the QS-21 saponin adjuvant in subunit vaccine formulations. In the current study, experimental subunit vaccine formulations containing recombinant p55-gag or gp120-%%%env%%% %%%proteins%%% from the mac251 strain of the simian immunodeficiency virus (SIV-mac251) and the QS-21 adjuvant were used to immunize rhesus macaques. These formulations induced SIV gag- or env-specific cellular immunity that was detectable in vitro and included killer cell %%%activity%%%. The induction of killer cells required prior vaccination and the responses were antigen specific for the immunogens contained in the vaccine formulations. Autologous target cells were required to detect

these responses, suggesting genetic restriction, and effector cells appeared to be present in both the CD4+ and CD8+ T lymphocyte subpopulations. These data suggest that the vaccine-induced killer cell %%%activity%%% that was detected was mediated by both CD4+ and CD8+ lymphocytes. Despite the presence of these killer cells, all of the animals became infected with the SIV-mac251 on experimental challenge. These findings demonstrated that antigen-specific killer cell responses could be induced by a subunit vaccine formulated with the QS-21 saponin adjuvant. The characteristics of the responses suggested that the effector cells were T lymphocytes, expressing either CD4 or CD8. These data also demonstrated that these types of cellular immune responses could not protect rhesus macaques from infectious SIV-mac251 challenge.

11/7/162 (Item 23 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0007841372 BIOSIS NO.: 199192087143
FUNCTIONAL ANALYSIS OF HUMAN T-CELL LEUKEMIA VIRUS TYPE I REX-RESPONSE ELEMENT DIRECT RNA BINDING OF REX PROTEIN CORRELATES WITH IN-VIVO %%%ACTIVITY%%%
AUTHOR: BALLAUN C (Reprint); FARRINGTON G K; DOBROVNIK M; RUSCHE J; HAUBER J; BOHNLEIN E
AUTHOR ADDRESS: SANDOZ RESEARCH INSTITUTE, BRUNNERSTRASSE 59, A-1235 VIENNA, AUSTRIA**AUSTRIA
JOURNAL: Journal of Virology 65 (8): p4408-4413 1991
ISSN: 0022-538X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The human T-cell leukemia virus type I rex gene product plays a critical role in the expression of the retroviral structural proteins Gag and Env from incompletely spliced mRNAs. Rex protein acts through a cis element (rex-response element [RxRE]) which is located in the U3/R region of the 3' long terminal repeat and is present on all human T-cell leukemia virus type I-specific mRNAs. Two domains of the predicted secondary structure of the RxRE are crucially important for Rex action in vivo as measured by two assay systems. In vitro studies using highly purified recombinant Rex protein revealed a specific and direct interaction with radiolabeled RxRE sequences. The correlation between our in vivo results and the binding of Rex protein to mutant and wild-type RxRE sequences supports both the existence of the predicted secondary structure and the importance of this direct interaction with the cis-acting RNA sequence for Rex function in vivo.

11/7/163 (Item 24 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0007766375 BIOSIS NO.: 199192012146
IDENTIFICATION AND CHARACTERIZATION OF NOVEL HUMAN ENDOGENOUS RETROVIRAL SEQUENCES PREFERENTIALLY EXPRESSED IN UNDIFFERENTIATED EMBRYONAL CARCINOMA CELLS
AUTHOR: LA MANTIA G (Reprint); MAGLIONE D; PENGUE G; DI CRISTOFANO A; SIMEONE A; LANFRANCONE L; LANIA L
AUTHOR ADDRESS: DEP GENETICS GEN AND MOL BIOL, UNIV NAPLES, VIA MEZZOCANNONE 8, 80124 NAPLES, ITALY**ITALY
JOURNAL: Nucleic Acids Research 19 (7): p1513-1520 1991
ISSN: 0305-1048
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A novel endogenous retroviral sequence (ERV-9) has been isolated from a human embryonal carcinoma cDNA library by hybridization to a probe containing a recently described human repetitive element. DNA sequence analysis of the 4kb cDNA insert (pHE.1) revealed the presence of ORFs potentially coding for putative retrovirus-related gag, pol and %%%env%%%

%%%proteins%%%. Northern blot and RNase protection experiments showed that RNA homologous to the pHE.1 insert is detected only in embryonal carcinoma cells as a 8 kb mRNA, and its expression is negatively regulated during retinoic acid induced differentiation of the human teratocarcinoma cell line NT2/D1. Using a pol specific probe we have isolated a genomic locus containing the ERV-9 sequences. Characterization by restriction enzyme analysis and DNA sequencing allowed us to define LTR-like sequences, that are composed by a complex array of subrepetitive elements. In addition we show that ERV-9 LTR sequences are capable to drive expression of linked CAT gene in a cell specific manner as LTR promoter %%%activity%%% has been detected only in NT2/D1 cells.

11/7/164 (Item 25 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0007628764 BIOSIS NO.: 199191011655
PRODUCTION OF A NON-FUNCTIONAL NEF PROTEIN IN HUMAN IMMUNODEFICIENCY VIRUS TYPE 1-INFECTED CEM CELLS
AUTHOR: LAURENT A G (Reprint); HOVANESSIAN A G; RIVIERE Y; KRUST B; REGNAULT A; MONTAGNIER L; FINDELI A; KIENY M P; GUY B
AUTHOR ADDRESS: UNITE ONCOLOGIE VIRALE, INST PASTEUR, 25 RUE DU DR ROUX, 75724 PARIS, FR**FRANCE
JOURNAL: Journal of General Virology 71 (10): p2273-2282 1990
ISSN: 0022-1317
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The nef gene product of the human immunodeficiency virus (HIV) is suggested to be a negative factor involved in down-regulating viral expression by a mechanism in which the correct conformation of the nef protein is essential. The nef protein expressed by vaccinia virus recombinants is phosphorylated by protein kinase C. We investigated the synthesis of the nef protein and its state of phosphorylation during HIV-1 infection of a T4 cell line (CEM cells). Maximum synthesis of viral proteins occurred 3 days after infection, when more than 90% of cells were producing viral proteins. The synthesis of the nef protein was detected in parallel with the env and gag proteins. As expected, the nef protein was myristylated but not phosphorylated, and its half-life was less than 1 h. By the use of the polymerase chain reaction technique, we isolated and sequenced the nef gene of this HIV-1 stock. Two significant mutations were observed. Firstly, threonine, at amino acid number 15, the site of phosphorylation by protein kinase C, was mutated into an alanine, and secondly aspartic acid of the tetrapeptide WRFD, which is probably involved in GTP binding, was mutated into an asparagine. The mutated nef gene was expressed in a vaccinia virus system, in which it was not phosphorylated and its half-life was dramatically reduced compared to the wild-type nef gene product. Furthermore, down-regulation of CD4 cell surface expression was no longer affected by the mutated nef gene. These results emphasize that phosphorylation of the nef protein provides an efficient test to monitor its biological %%%activity%%%.

11/7/165 (Item 26 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0007208724 BIOSIS NO.: 199089126615
ANALYSIS OF ANTIBODY RESPONSES TO PHENOTYPICALLY DISTINCT LENTIVIRUSES
AUTHOR: KAJIKAWA O (Reprint); LAIRMORE M D; DEMARTINI J C
AUTHOR ADDRESS: DEP PATHOL, COLL VET MED AND BIOMED SCI, COLO STATE UNIV, FORT COLLINS, COLO 80523, USA**USA
JOURNAL: Journal of Clinical Microbiology 28 (4): p764-770 1990
ISSN: 0095-1137
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: To define the immune responses against phenotypically and

pathogenically distinct lentiviruses, we used an immunoblotting assay to study antibodies to viral proteins of ovine lentivirus (OvLV) in 16 experimentally and 12 naturally infected sheep. Two distinct phenotypes of OvLV were used to experimentally infect lambs: strain 85/34, a "rapid/high" isolate which rapidly induced lysis in infected primary macrophage cultures and replicated to relatively high titers, and strains 84/28 and 85/14, "slow/low" isolates which induced slowly progressive syncytia with minimal lysis in vitro and replicated only to low titers in the same cell type. Serum antibodies against four major viral structural proteins, gp105, p25, p16, and p14, were detected. In a longitudinal study of experimentally infected lambs, the antibody to p25 (major gag protein) usually appeared first (average, about 3 weeks postinoculation [p.i]) and was followed in about 2 weeks by p16, p14, and gp105 almost simultaneously. Six of 16 animals did not develop anti-p14 antibody by the time of necropsy at 9 to 29 weeks p.i. Two of 10 lambs which developed antibody to p14 had the antibody only transiently from 3 to 8 or 13 weeks p.i. and lost it by the time of necropsy at 21 or 22 weeks p.i. In contrast, antibodies to the other three structural proteins remained fairly constant until the time of necropsy. There were differences in the antibody responses of the experimentally infected lambs to the two phenotypes of OvLV. Seven of 10 (70%) lambs which were inoculated with the rapid/high strain developed antibody to p14, whereas only 17% of the lambs inoculated with the slow/low strains had antibody to this protein. In the longitudinal study, no decline was observed in the %%%activity%%% of any specific antibody such as that which occurs with anti-p24 antibody in human immunodeficiency virus infection, except in the case of anti-p14 antibody in two lambs. There were no significant differences in antibody titers against p25, p16, and p14 in final blood samples between rapid/high virus- and slow/low virus-infected groups. However, the rapid/high virus-infected group developed a fivefold-higher geometric mean titer of anti-env product (gp105) antibody than did the slow/low virus-infected group (P .ltoreq. 0.1). Antibody titers to all major structural proteins, except p14, in the naturally infected sheep were markedly lower than those in experimentally induced OvLV infections (P .ltoreq. 0.01). The failure of the slow/low virus-infected group to develop anti-p14 antibody may suggest diminished viral replication in vivo or a failure of the host to recognize p14 in the slow/low virus-infected group. Since the geometric mean antibody titer to gp105 was threefold higher in lambs with lymphoid interstitial pneumonia than in those without lesions and since no differences were observed in the titers of other antiviral antibodies between these groups, we found no evidence to suggest that levels of such antibodies correlated with protection from OvLV-induced disease.

11/7/166 (Item 27 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0003982116 BIOSIS NO.: 198376073551
NUCLEOTIDE SEQUENCE AND ORGANIZATION OF THE TRANSFORMING REGION AND LARGE TERMINAL REDUNDANCIES OF AVIAN MYELOBLASTOSIS VIRUS
AUTHOR: PAPAS T S (Reprint); RUSHLOW K E; WATSON D K; LAUTENBERGER J A; PERBAL B; BALUDA M E; REDDY E P
AUTHOR ADDRESS: LAB MOLECULAR ONCOLOGY, NATL CANCER INST, BETHESDA, MD 20205, USA**USA
JOURNAL: Journal of Cellular Biochemistry 20 (2): p95-104 1982
ISSN: 0730-2312
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Avian myeloblastosis virus (AMV) is a replication-defective acute leukemia virus, reguiring a helper virus to provide the viral proteins essential for synthesis of new infectious virus. The genome of the AMV has undergone a sequence substitution in which a portion of the region normally coding for the %%%env%%% %%%protein%%% was replaced by chicken cellular sequences. These latter sequences are essential for the transforming %%%activity%%% of the virus. The complete nucleotide sequence of this region was determined. Examination of the AMV oncogenic sequence revealed an open reading frame starting with the initiation

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  codon ATG within the acquired cellular sequences and terminating with the
  triplet TAG at a point 33 nucleotides into helper viral sequence to the
  right of helper-viral-cellular junction. The stretch of 795 nucleotides
  would code for a protein of 265 amino acids with a MW of 30,000 daltons.
  The 11 amino acids at the carboxy terminus of such a protein would be
  derived from the env gene of helper virus.
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              $3.96  18 Type(s) in Format  7
           $3.96  18 Types
    $20.46  Estimated cost File155
          $24.74    4.193 DialUnits File5
             $71.75  35 Type(s) in Format  7
              $0.00  17 Type(s) in Format 66
          $71.75  52 Types
    $96.49  Estimated cost File5
            OneSearch, 2 files,  9.045 DialUnits FileOS
     $5.86  TELNET
   $122.81  Estimated cost this search
   $122.83  Estimated total session cost   9.360 DialUnits
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      Set  Items  Description
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? s retrovirus()genome
          16615  RETROVIRUS
         115525  GENOME
      S1      74  RETROVIRUS()GENOME
? s s1 and review
             74  S1
         553651  REVIEW
      S2      4  S1 AND REVIEW
? t s2/7/1-4

 2/7/1
DIALOG(R)File   5:Biosis Previews(R)
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0005915229   BIOSIS NO.: 198835012334
ORGANIZATION OF THE %%%RETROVIRUS%%% %%%GENOME%%%
AUTHOR: ORTEGA CALVO J J (Reprint); ORTEGA CALVO M
AUTHOR ADDRESS: INSTITUTO DE RECURSOS NATURALES Y AGROBIOLOGIA DE SEVILLA,
  CSIC
JOURNAL: Revista Clinica Espanola  182 (2): p107-113 1988
ISSN: 0014-2565
DOCUMENT TYPE: Meeting
RECORD TYPE: Citation
LANGUAGE: SPANISH


 2/7/2
DIALOG(R)File   5:Biosis Previews(R)
(c) 2006 BIOSIS. All rts. reserv.

0004501642   BIOSIS NO.: 198529030541
REPRODUCTION AND ASSEMBLY OF ONCOVIRUSES
AUTHOR: SHERBAN S D (Reprint); STRUK V I
AUTHOR ADDRESS: RE KAVETSKII INST PROBL ONCOL, ACAD SCI UKR SSR, KIEV, USSR
  **USSR
JOURNAL: Eksperimental'naya Onkologiya  6 (5): p3-9 1984
ISSN: 0204-3564
DOCUMENT TYPE: Article
RECORD TYPE: Citation
LANGUAGE: RUSSIAN


 2/7/3
DIALOG(R)File   5:Biosis Previews(R)
(c) 2006 BIOSIS. All rts. reserv.

0003367716   BIOSIS NO.: 198222011659
REGULATION OF EXPRESSION OF THE INTEGRATED %%%RETROVIRUS%%% %%%GENOME%%%
AUTHOR: WEINBERG R A (Reprint); STEFFEN D L
AUTHOR ADDRESS: CENT CANCER RES DEP BIOL, MASS INST TECHNOL, CAMBRIDGE,
  MASS 02139, USA**USA
JOURNAL: Journal of General Virology  54 (1): p1-8 1981
ISSN: 0022-1317
DOCUMENT TYPE: Article
RECORD TYPE: Citation
LANGUAGE: ENGLISH


 2/7/4
DIALOG(R)File   5:Biosis Previews(R)
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0001973979   BIOSIS NO.: 197764072483
ONCORNAVIRUSES GENOME PROPERTIES OF VIRAL RNA IN VIRIONS AND CELLS
AUTHOR: LARSEN C J
JOURNAL: Pathologie Biologie  25 (4): p247-273 1977
ISSN: 0369-8114
DOCUMENT TYPE: Article
```

RECORD TYPE: Abstract
LANGUAGE: Unspecified

ABSTRACT: The 1st part of this %%%review%%% on the oncornavirus (%%%retrovirus%%%) %%%genome%%% deals with the structural features of the 60-70S RNA and its subunits and other cellular RNA which are present in the viruses. The 2nd part describes the viral RNA species which were found in various cell systems including infected producer cells, transformed and non-producer cells, normal and inducible cells. A special part is devoted to viral RNA isolated from human cancer cells.

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? s retrovirus
      S3   16615  RETROVIRUS
? s clon?
      S4  324382  CLON?
? s s3 and s4
           16615  S3
          324382  S4
      S5    2270  S3 AND S4
? s map and s5
           84335  MAP
            2270  S5
      S6      57  MAP AND S5
? s s6 and review
              57  S6
          553651  REVIEW
      S7       0  S6 AND REVIEW
? t s6/7/25-35
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6/7/25
DIALOG(R)File 5:Biosis Previews(R)

0007968908 BIOSIS NO.: 199242071799
BIOLOGICAL AND MOLECULAR STUDIES ON ENDOGENOUS %%%RETROVIRUS%%%-LIKE GENES IN CHINESE HAMSTER CELL LINES
BOOK TITLE: INTERNATIONAL ASSOCIATION OF BIOLOGICAL STANDARDIZATION (ED.). DEVELOPMENTS IN BIOLOGICAL STANDARDIZATION, VOL. 75. VIROLOGICAL ASPECTS OF THE SAFETY OF BIOLOGICAL PRODUCTS; SYMPOSIUM, LONDON, ENGLAND, UK, NOVEMBER 8-9, 1990. IX+275P. S. KARGER AG: BASEL, SWITZERLAND; NEW YORK, NEW YORK, USA. ILLUS
AUTHOR: EMANOIL-RAVIER R (Reprint); HOJMAN F; SERVENAY M; LESSER J; BERNARDI A; PERIES J
AUTHOR ADDRESS: UPR A0043 CNRS "RETROVIRUS RETROTRASPOSONS DES VERTEBRES", HOP SAINT-LOUIS, 1 AVE CLAUDE-VELLEFAUX, F-75010 PARIS, FR**FRANCE
SERIES TITLE: Developments in Biological Standardization p113-122 1991
ISSN: 0301-5149 ISBN: 3-8055-5467-2
DOCUMENT TYPE: Book; Meeting
RECORD TYPE: Citation
LANGUAGE: ENGLISH

6/7/26
DIALOG(R)File 5:Biosis Previews(R)

0007818401 BIOSIS NO.: 199192064172
CELLULAR TRANSCRIPTS ENCODED AT A LOCUS WHICH PERMITS %%%RETROVIRUS%%% EXPRESSION IN MOUSE EMBRYONIC CELLS
AUTHOR: PETERSEN R (Reprint); SOBEL S; WANG C-T; JAENISCH R; BARKLIS E
AUTHOR ADDRESS: DEP MICROBIOLOGY, MAIL CODE L220, 3181 SW SAM JACKSON PK RD, PORTLAND, OREG 97201, USA**USA
JOURNAL: Gene (Amsterdam) 101 (2): p177-184 1991
ISSN: 0378-1119
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Three independent recombinant retroviruses have been activated on insertion into the F2 locus of mouse F9 embryonal carcinoma cells. Each provirus has integrated downstream from the cellular F2 promoter, which is active in transient transfection assays using a chloramphenicol

acetyltransferase reporter enzyme. The F2 promoter drives expression of a series of related transcripts in F9 and 3T3 cells, and a single 450-nt transcript in mouse tissues. F2 homologous sequences have been detected in the genomes of all mammalian species tested, and the 450-nucleotide (nt) F2 transcript is expressed in rat and human cells. Three pairs of differently sized F2 cDNA %%%clones%%% have been isolated and analyzed. The largest %%%clones%%% possesses two 199-nt 98.5% identical repeats, one of which is present in the smaller %%%clones%%%, as well as the major 450-nt transcript. Activated proviral integration sites %%%map%%% to introns of the largest F2 cDNA %%%clone%%%. While none of the F2 cDNA contains a long open reading frame or homology to databank sequences, evidence suggests that the F2 locus encodes a constitutive function required at high levels, or represents an expressed but nonfunctional, single-copy element, conserved among mammals.

6/7/27
DIALOG(R)File 5:Biosis Previews(R)

0007742876 BIOSIS NO.: 199191125767
LOCALIZATION OF THE HUMAN GENE ALLOWING INFECTION BY GIBBON APE LEUKEMIA VIRUS TO HUMAN CHROMOSOME REGION 2Q11-Q14 AND TO THE HOMOLOGOUS REGION ON MOUSE CHROMOSOME 2
AUTHOR: KAELBLING M (Reprint); EDDY R; SHOWS T B; COPELAND N G; GILBERT D J ; JENKINS N A; KLINGER H P; O'HARA B
AUTHOR ADDRESS: MOLECULAR BIOLOGY RESEARCH SECTION, LEDERLE LABORATORIES, AMERICAN CYANAMID COMPANY, PEARL RIVER, NY 10965, USA**USA
JOURNAL: Journal of Virology 65 (4): p1743-1747 1991
ISSN: 0022-538X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: %%%Retrovirus%%% receptors remain a largely unexplored group of proteins. Of the receptors which allow infection of human and murine cells by various retroviruses, only three have been identified at the molecular level. These receptors include CD4 for human immunodeficiency virus, Rec-1 for murine ecotropic virus, and GLVR1 for gibbon ape leukemia virus. These three proteins show no homology to one antoher at the DNA or protein level. Therefore, work to date has not shown any general relationship or structural theme shared by retroviral receptors. Genes for two of these receptors (CD4 and Rec-1) and several others which have not yet been %%%cloned%%% have been localized to specific chromosomes. In order to assess the relationship between GLVR1 and other retroviral receptors, we mapped the chromosome location of GLVR1 in human and mouse. GLVR1 was found to %%%map%%% to human chromosome 2q11-q14 by in situ hybridization and somatic-cell hybrid analysis. This location is distinct from those known for receptors for retroviruses infecting human cells. Glvr-1 was then mapped in the mouse by interspecies backcrosses and found to %%%map%%% to chromosome 2 in a region of linkage conservation with human chromosome 2. This mouse chromosome carries Res-2, the likely receptor for M813, a %%%retrovirus%%% derived from a feral Asian mouse. These data raise the interesting possibility that Rec-2 and Glvr-1 are structurally related.

6/7/28
DIALOG(R)File 5:Biosis Previews(R)

0007667085 BIOSIS NO.: 199191049976
MOLECULAR %%%CLONING%%% AND CHARACTERIZATION OF %%%RETROVIRUS%%%-LIKE INTRACISTERNAL TYPE A PARTICLE GENES IAP PRESENT IN THE CHINESE HAMSTER GENOME
AUTHOR: SERVENAY M (Reprint); KUPIEC J-J; PERIES J; EMANOIL-RAVIER R
AUTHOR ADDRESS: UPR A0043 CNRS, "RETROVIRUS ET RETROTRANSPOSONS DE VERTEBRES", HOP SAINT-LOUIS, 1 AVENUE CLAUDE VELIEFAUX, 75010 PARIS, FRANCE**FRANCE
JOURNAL: Virus Genes 4 (4): p351-358 1990
ISSN: 0920-8569

DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Endogenous %%%retrovirus%%%-like sequences that are homologous to the multigenic murine and Syrian hamster intracisternal type A particle (IAP) genes can be detected in very few copies in the Chinese hamster (CH) genome. They were %%%cloned%%% from a CHO gene library and two recombinants, harboring the major IAP-like DNA genes characterized by Southern blot hybridization after DNA digestion with several restriction enzymes. The IAP DNA inserts of the two %%%clones%%% and analyzed wer 4.70 and 8.04 kb respectively, allowing us to construct a physical %%%map%%% of our Chinese hamster %%%clone%%% that represents an almost complete IAP element.

6/7/29
DIALOG(R)File 5:Biosis Previews(R)

0007243580 BIOSIS NO.: 199090028059
GENETIC MAPPING OF A %%%CLONED%%% SEQUENCE RESPONSIBLE FOR SUSCEPTIBILITY TO ECOTROPIC MURINE LEUKEMIA VIRUSES
AUTHOR: KOZAK C A (Reprint); ALBRITTON L M; CUNNINGHAM J
AUTHOR ADDRESS: NATL INST ALLERGY INFECTIOUS DISEASES, BETHESDA, MD 20892, USA**USA
JOURNAL: Journal of Virology 64 (6): p3119-3121 1990
ISSN: 0022-538X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A mouse cDNA that confers susceptibility to ecotropic murine leukemia viruses following transfection into human EJ cells has been %%%cloned%%% and sequenced. We show that this sequence is likely to be Rec-1, the chromosome 5 locus originally defined by studies with somatic cell hybrids as responsible for virus susceptibility, and provide a specific chromosomal %%%map%%% position for this locus by analysis of an interspecies backcross. This locus maps in the distal region of chromosome 5 and is thus not within the cluster of %%%retrovirus%%% -related genes near the centromere.

6/7/30
DIALOG(R)File 5:Biosis Previews(R)

0007102837 BIOSIS NO.: 199089020728
MOLECULAR %%%CLONING%%% OF A TYPE D %%%RETROVIRUS%%% FROM HUMAN CELLS PMFV AND ITS HOMOLOGY TO SIMIAN ACQUIRED IMMUNODEFICIENCY TYPE D RETROVIRUSES
AUTHOR: KRAUSE H (Reprint); WUNDERLICH V; UCKERT W
AUTHOR ADDRESS: AKAD WISSENSCHAFTEN DDR, ZENTRALINST KREBSFORSCHUNG, BEREICH VIROL, ROBERT-ROESSLE-STR 80, BERLIN DDR-1115, GDR**EAST GERMANY
JOURNAL: Virology 173 (1): p214-222 1989
ISSN: 0042-6822
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Unintegrated circular proviral DNA of a type D %%%retrovirus%%% (PMFV) isolated from a permanent human cell line was molecularly %%%cloned%%% in the bacteriophage vector L47.1 and subcloned in the plasmid vector pGEM-2. A restriction endonuclease %%%map%%% of PMFV DNA was established using 10 different enzymes for single and multiple digestions of closed circular and %%%cloned%%% DNA molecules. By restriction endonuclease analysis %%%cloned%%% PMFV DNA represented full-length viral DNA with one long terminal repeat (LTR). The comparison of the physical %%%map%%% of %%%cloned%%% PMFV to those of other %%%cloned%%% type D retroviruses revealed closet homology to the %%%map%%% of %%%retrovirus%%% D/New England (pD398) and SAIDS %%%retrovirus%%% type 1 (SRV-1). The relatedness of PMFV to further type

D retroviruses (Mason-Pfizer monkey virus, MPMV; SAIDS %%%retrovirus%%% type 2, SRV-2) was also demonstrated by cross-hybridization of %%%cloned%%% DNAs under different stringencies (i) using full-length genomic probes of PMFV, MPMV, and SRV-2 and (ii) by DNA sequence analysis of regions of the group specific antigen (gag) protease (prt), polymerase (pol), and envelope (env) genes.

6/7/31
DIALOG(R)File 5:Biosis Previews(R)

0006799782 BIOSIS NO.: 198988114897
DETECTION OF HUMAN SEQUENCE RELATED TO THE SQUIRREL MONKEY %%%RETROVIRUS%%%
AUTHOR: ASONUMA H (Reprint)
AUTHOR ADDRESS: DEP BIOCHEM, CANCER INST, OKAYAMA UNIV MED SCH, OKAYAMA 700, JPN**JAPAN
JOURNAL: Okayama Igakkai Zasshi 101 (5-6): p423-436 1989
ISSN: 0030-1558
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: JAPANESE

ABSTRACT: Squirrel monkey %%%retrovirus%%% (SMRV) is an endogenous type D %%%retrovirus%%% of the squirrel monkey, a New World primate. Southern hybridization with %%%cloned%%% SMRV-H revealed that 30 .apprx. 40 copies of SMRV proviral DNA are present in the squirrel monkey genome and the majority have almost the same physical %%%map%%% as that of the %%%cloned%%% SMRV-H. SMRV-related sequences in the human genome were sought using the same method with various %%%cloned%%% SMRV-H DNA fragments under conitions of relaxed stringency. The discrete restriction fragments were frequently detected in the DNA from normal humans with the LTR and parts of gag and env as probes. Since SMRV LTR has very little homology with the LTRs of other retroviruses, the fragments detected with the LTR probe were characterized as SMRV-related human sequences. SMRV LTR-related sequences were also detected in the African green monkey and chicken, but not in the salmon, mouse, or dog. In conclusion, SMRV-related sequences are present in human DNA, and some of them might represent endogenous retroviral sequences of human DNA.

6/7/32
DIALOG(R)File 5:Biosis Previews(R)

0006262390 BIOSIS NO.: 198886102311
PLASMID TRANSFECTION WITH %%%RETROVIRUS%%% PROMOTOR DISTRIBUTION OF SEQUENCES IN THE GENOME OF INDUCED TUMORS
AUTHOR: GLAZACHEV V A (Reprint); TOPOL' L Z; TATOSYAN A G
AUTHOR ADDRESS: ALL-UNION ONCOL SCI CENT, ACAD MED SCI USSR, MOSCOW 115478, USSR**USSR
JOURNAL: Molekulyarnaya Biologiya (Moscow) 22 (2): p506-516 1988
ISSN: 0026-8984
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: RUSSIAN

ABSTRACT: The structure of the integration site of plasmid with LTR of Rous sarcoma virus (pLTR1,5) in the genome of nude mice tumors, induced as a result of NIH3T3 cell implantation, cotransfected by pLTR1,5 with the DNA of malignant human glioma cells, carrying amplified c-Ha-ras genome, has been studied. The restriction %%%map%%% of the investigated region of the cell genome was obtained. Molecular %%%cloning%%% of the integrated plasmid and adjacent cell sequences has been carried out. It was shown that the exogenic vector in the DNA of the tumor cells is included in BamHI structure of the repeat of mice genome.

6/7/33
DIALOG(R)File 5:Biosis Previews(R)

0006251215 BIOSIS NO.: 198886091136
AVIAN NEPHROBLASTOMAS INDUCED BY A %%%RETROVIRUS%%% MAV-2 LACKING ONCOGENE I. CONSTRUCTION OF MAV-1 AND MAV-2 PROVIRAL RESTRICTION MAPS AND PREPARATION OF SPECIFIC PROVIRAL MOLECULAR SUBCLONES
AUTHOR: PECENKA V (Reprint); DVORAK M; TRAVNICEK M
AUTHOR ADDRESS: INST MOL GENET, CZECHOSLOVAK ACAD SCI, 166 37 PRAHA** CZECHOSLOVAKIA
JOURNAL: Folia Biologica (Prague) 34 (3): p129-146 1988
ISSN: 0015-5500
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A 9.8 kb DNA fragment containing the complete MAV-1 provirus was recloned from the recombinant bacteriophage .lambda.311411 (Perbal et al., 1985) into the plasmid pAT153. A detailed and precise restriction %%%map%%% of the obtained %%%clone%%% (pAT-MAV-1) was constructed. From compilation of this %%%map%%% and the known sequence of a variable portion of the MAV-2 env gene was a restriction %%%map%%% of MAV-2 deduced. Knowledge of the detailed pAT-MAV-1 %%%map%%% facilitated the preparation of five specific proviral subclones: pAT-U3 and pUC-U3 (both contain the U3 domain of the proviral LTR, which is MAV-specific and displays no homology with other hitherto known retroviruses including avian endogenous proviruses), pUC-RU5 (containing the R and U5 domains of the proviral LTR), pUC-UT5 (containing untranslated sequences flanking the 5' LTR), and pUC-UT3 (containing untranslated sequences flanking the 3' LTR). Thus tools for analysis of integrated MAV-2 proviruses in nephroblastomas induced by this virus were formed.

0006242349 BIOSIS NO.: 198886082270
ALTERATIONS IN THE U-3 REGION OF THE LONG TERMINAL REPEAT OF AN INFECTIOUS THYMOTROPIC TYPE B %%%RETROVIRUS%%%
AUTHOR: BALL J K (Reprint); DIGGELMANN H; DEKABAN G A; GROSSI G F; SEMMLER R; WAIGHT P A; FLETCHER R F
AUTHOR ADDRESS: DEP BIOCHEM, UNIV WESTERN ONT, LONDON, ONT N6A 5C1**CANADA
JOURNAL: Journal of Virology 62 (8): p2985-2993 1988
ISSN: 0022-538X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: We isolated and characterized a type B thymotropic %%%retrovirus%%% (DMBA-LV) which is highly related to mouse mammary tumor virus (MMTV) isolates and which induces T-cell thymomas with a high incidence and a very short latent period. Regions of nonhomology between the DMBA-LV genome and the MMTV genome were identified by heteroduplex mapping and nucleotide sequence studies. In the electron microscope heteroduplex mapping studies the EcoRI-generated 5' and 3' fragments of the DMBA-LV genome were compared with the corresponding fragments of the MMTV (C3H and GR) genome isolated from mammary tumors. The results indicated that DMBA-LV contained a region of nonhomologous nucleotide sequences in the 3' half of the U3 region of the long terminal repeat (LTR). Nucleotide sequence studies confirmed these results and showed that in this region 440 nucleotides of the MMTV (C3H) sequences were deleted and substituted with a segment of 122 nucleotides. This substituted segment in the form of a tandem repeat structure contained nucleotide sequences derived exclusively from sequences which flanked the substitution loop. The distal glucocorticoid regulatory element was unaltered, and two additional copies of the distal glucocorticoid regulatory element-binding site were present in the substituted region. The restriction endonuclease %%%map%%% of the reconstructed molecular %%%clone%%% of DMBA-LV was identical to that corresponding to unintegrated linear DMBA-LV DNA present in DMBA-LV-induced tumor cell lines. Since the nucleotide sequences of the LTRs present in four different DMBA-LV proviral copies isolated from a single thymoma were

identical, we concluded that they were derived from the same parental virus and that this type B %%%retrovirus%%% containing an alteration in the U3 region of its LTR could induce thymic lymphomas. Thus, DMBA-LV represents the first example of a productively replicating type B %%%retrovirus%%% that contains an LTR modified in the U3 region and that has target cell and disease specificity for T cells.

6/7/35
DIALOG(R)File 5:Biosis Previews(R)

0005703635 BIOSIS NO.: 198784057784
ONCOGENESIS BY MOLONEY MURINE LEUKEMIA VIRUS
AUTHOR: TSICHLIS P N (Reprint)
AUTHOR ADDRESS: FOX CHASE CANCER CENTER, PHILADELPHIA, PA 19111, USA**USA
JOURNAL: Anticancer Research 7 (2): p171-180 1987
ISSN: 0250-7005
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Moloney murine leukemia virus (MoMuLV) is a %%%retrovirus%%% which lacks an oncogene. It is, however, highly oncogenic in rats and mice, in whom it induces thymic lymphomas. These lymphomas are %%%clonal%%% tumors and appear four to six months following virus inoculation. Although provirus integration is random in virus infected non-tumor cells, it shows regional specificity in these tumors, thus suggesting that insertional mutagenesis may play an important role in tumor induction and progression. Our studies have revealed four common DNA regions for provirus insertion in these tumors (Mlvi-1, Mlvi-2, Mlvi-3 and c-Myc), while studies from other laboratories have revealed two additional ones (pvt-1/mis-1 and pim-1). Mlvi-1, Mlvi-2 and Mlvi-3 represent three independent logi since there is no homology between the molecular %%%clones%%% that identify them and they %%%map%%% on different rat chromosomes. It is interesting however that two of them (Mlvi-1 and Mlvi-2), as well as pvt-1/mis-1, %%%map%%% to mouse chromosome 15 which is known to become trisomic in murine thymic lymphomas. In addition to the specificity of provirus integration, tumor induction is also associated with amplification of the proviral DNA. This amplification may be favored during oncogenesis because cells that carry insertion mutations in multiple oncogenes may exhibit growth advantage over cells in which only single insertion mutations have occurred. This could happen because the effect of these mutations may be additive or because there is a synergistic relationship between multile loci during oncogenesis. This was indeed suggested by the appearance of concerted provirus insertions in Mlvi-1 and Mlvi-2. Alternatively, the amplification of the provirus during tumor induction may be selected because it provides for elevated levels of viral gene products that participate in the process of oncogenesis. Such products may be coded by sequences in the gag/pol region. We indeed present evidence here for a 2 kb tumor specific gag/pol transcript which is expressed in these thymomas. Our analysis of Mlvi-1 and Mlvi-2 has revealed the following. Mlvi-1 contains at least one open reading frame which is conserved among species and which preliminary evidence indicates may be expressed in the thymomas. Additionally Mlvi-1 appears to be present in more than one copy per haploid genome in both rats and humans. In Mlvi-2 we have shown the presence of a transcribed region downstream from the cluster of the integrated proviruses in the MoMuLV induced thymic lymphomas. However this transcript is expressed mostly in rat embryo fibroblasts. The final outcome of oncogenesis, i.e. the formation of a detectable tumor, is due to the interplay of multiple events that are related to both tumor induction and tumor progression. One of the events associated with tumor progression is recombination between homologous DNA sequences. In one example of such an event recombination occurred between the long terminal repeat (LTR) sequences of two integrated proviruses, one of which was inserted 5' to the c-myc protooncogene. This resulted in the splicing of a distant located DNA sequence next to c-myc.
? ds

Set Items Description

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S1          74   RETROVIRUS()GENOME
S2           4   S1 AND REVIEW
S3       16615   RETROVIRUS
S4      324382   CLON?
S5        2270   S3 AND S4
S6          57   MAP AND S5
S7           0   S6 AND REVIEW
? s s3 and review
           16615  S3
          553651  REVIEW
      S8     922  S3 AND REVIEW
? s s8 and genome
             922  S8
          115525  GENOME
      S9     115  S8 AND GENOME
? s s9 and map
             115  S9
           84335  MAP
     S10       0  S9 AND MAP
? t s9/7/50-70

 9/7/50
DIALOG(R)File   5:Biosis Previews(R)
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0013707350   BIOSIS NO.: 200200300861
Mechanisms of retroviral recombination
BOOK TITLE: Annual %%%Review%%% of Genetics
AUTHOR: Negroni Matteo (Reprint); Buc Henri
BOOK AUTHOR/EDITOR: Campbell Allan (Editor); Anderson Wyatt W (Editor);
  Jones Elizabeth W (Editor)
AUTHOR ADDRESS: Unite de Regulation Enzymatique des Activites Cellulaires,
  FRE 2364-CNRS, Institut Pasteur, 25-28 rue du Dr. Roux, 75724, Paris,
  Cedex 15, France**France
SERIES TITLE: Annual %%%Review%%% of Genetics  35 p275-302 2001
MEDIUM: print
BOOK PUBLISHER: Annual Reviews {a}, 4139 El Camino Way, Palo Alto, CA,
                94303-0139, USA
ISSN: 0066-4197  ISBN: 0-8243-1235-X  (cloth)
DOCUMENT TYPE: Book; Book Chapter
RECORD TYPE: Citation
LANGUAGE: English


 9/7/51
DIALOG(R)File   5:Biosis Previews(R)
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0013645244   BIOSIS NO.: 200200238755
Gene therapy: Optimising DNA delivery to the nucleus
AUTHOR: Johnson-Saliba Melanie; Jans David A (Reprint)
AUTHOR ADDRESS: Nuclear Signalling Laboratory, Division of Biochemistry and
  Molecular Biology, John Curtin School of Medical Research, Australian
  National University, Canberra, ACT, 0200, Australia**Australia
JOURNAL: Current Drug Targets  2 (4): p371-399 December, 2001 2001
MEDIUM: print
ISSN: 1389-4501
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Citation
LANGUAGE: English


 9/7/52
DIALOG(R)File   5:Biosis Previews(R)
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0013578669   BIOSIS NO.: 200200172180
The genetics of the target tissue in rheumatoid arthritis
AUTHOR: Corr Maripat (Reprint); Firestein Gary S
AUTHOR ADDRESS: UCSD School of Medicine, 9500 Gilman Drive, La Jolla, CA,
  92093-0663, USA**USA
```

JOURNAL: Rheumatic Disease Clinics of North America 28 (1): p79-94
February, 2002 2002
MEDIUM: print
ISSN: 0889-857X
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Citation
LANGUAGE: English

9/7/53
DIALOG(R)File 5:Biosis Previews(R)

0013407600 BIOSIS NO.: 200200001111
Evidence for genomic rearrangements mediated by human endogenous retroviruses during primate evolution
AUTHOR: Hughes Jennifer F; Coffin John M (Reprint)
AUTHOR ADDRESS: Department of Molecular Biology and Microbiology and Program in Genetics, Tufts University School of Medicine, 136 Harrison Avenue, Boston, MA, 02111, USA**USA
JOURNAL: Nature Genetics 29 (4): p487-489 December, 2001 2001
MEDIUM: print
ISSN: 1061-4036
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Human endogenous retroviruses (HERVs), which are remnants of past retroviral infections of the germline cells of our ancestors, make up as much as 8% of the human %%%genome%%% and may even outnumber genes. Most HERVs seem to have entered the %%%genome%%% between 10 and 50 million years ago, and they comprise over 200 distinct groups and subgroups. Although repeated sequence elements such as HERVs have the potential to lead to chromosomal rearrangement through homologous recombination between distant loci, evidence for the generality of this process is lacking. To gain insight into the expansion of these elements in the %%%genome%%% during the course of primate evolution, we have identified 23 new members of the HERV-K (HML-2) group, which is thought to contain the most recently active members. Here we show, by phylogenetic and sequence analysis, that at least 16% of these elements have undergone apparent rearrangements that may have resulted in large-scale deletions, duplications and chromosome reshuffling during the evolution of the human %%%genome%%%.

9/7/54
DIALOG(R)File 5:Biosis Previews(R)

0013368272 BIOSIS NO.: 200100540111
Reverse transcription of retroviruses and LTR retrotransposons
AUTHOR: Wilhelm M; Wilhelm F-X (Reprint)
AUTHOR ADDRESS: Unite Propre de Recherche 9002, Institut de Biologie Moleculaire et Cellulaire, Centre National de la Recherche Scientifique, 15 rue Rene Descartes, 67084, Strasbourg Cedex, France**France
JOURNAL: CMLS Cellular and Molecular Life Sciences 58 (9): p1246-1262
August, 2001 2001
MEDIUM: print
ISSN: 1420-682X
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Retroelements are mobile genetic entities that replicate via reverse transcription of a template RNA. A key component to the life cycle of these elements is the enzyme reverse transcriptase (RT), which copies the single-stranded genomic RNA of the element into a linear double-stranded DNA that is ultimately integrated into the host %%%genome%%% by the element-encoded integrase. RT is a multifunctional enzyme which possesses RNA-dependent and DNA-dependent DNA polymerase activities as well as RNase H activity that specifically degrades the RNA

strand of RNA-DNA duplexes. At some stages of the replication a strand-displacement activity of RT is also necessary. All activities are essential for the conversion of single-stranded genomic RNA into the double-stranded preintegrative DNA. This %%%review%%% focuses on the role of RT in the different steps of the replication process of retroelements. The features of retrotransposon replication which differ from the retroviral ones will be emphasized. In a second part of the %%%review%%%, the biochemical and enzymatic properties of two newly characterized retrotransposon RTs will be described. The role of the integrase domain in reverse transcriptase activity of some retroviral and retrotransposon RTs will be discussed.

9/7/55
DIALOG(R)File 5:Biosis Previews(R)

0013163607 BIOSIS NO.: 200100335446
Journey to the center of the cell
AUTHOR: Cullen Bryan R (Reprint)
AUTHOR ADDRESS: Department of Genetics, Howard Hughes Medical Institute, Duke University Medical Center, Durham, NC, 27710, USA**USA
JOURNAL: Cell 105 (6): p697-700 June 15, 2001 2001
MEDIUM: print
ISSN: 0092-8674
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Citation
LANGUAGE: English

9/7/56
DIALOG(R)File 5:Biosis Previews(R)

0013085901 BIOSIS NO.: 200100257740
[Retroviral elements in the chicken %%%genome%%%: An overview]
ORIGINAL LANGUAGE TITLE: Retrovirale Elemente im Huehnergenom: Ein Ueberblick
AUTHOR: Brade W (Reprint)
AUTHOR ADDRESS: LWK und TiHo Hannover, Johannssen-str. 10, 30159, Hannover, Germany**Germany
JOURNAL: Archiv fuer Gefluegelkunde 65 (2): p49-57 April, 2001 2001
MEDIUM: print
ISSN: 0003-9098
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: German

ABSTRACT: Retroviral elements or retroviruses have been found in all vertebrates investigated. The molecular basis is the copying of RNA into DNA during a stepp in the life cycle of each of exogenous organisms. This process is carried out by reverse transcriptase (RT), in most cases encoded by the retroelements but, in a few cases, such as the the retrotranscripts, "borrowed" from another retroelements. This article is designed to provide an overview on endogenous retroviruses respectively retroviral elements in the chicken %%%genome%%%. Endogenous retroviruses (ALVEs) - which are closely related to exogenous leukosis viruses (ALVs) - have been found in chicken genomes. More recently, at least three families more of endogenous %%%retrovirus%%%-like elements have been cloned. Expression of endogenous retroviruses can influence the host physiology and productivity. It is important therefore, to be able to establish the ALVE-element profiles of chicken quickly and accurately. The current method of choice for simple, quick and accurate typing is the polymerase chain reaction (PCR). In present time it is possible to list the assay protocols for 19 different ALVE-elementes, which can be used in new selection strategies.

9/7/57
DIALOG(R)File 5:Biosis Previews(R)

0012887361 BIOSIS NO.: 200100059200
Mechanisms of %%%retrovirus%%%-induced oncogenesis
AUTHOR: Sourvinos G; Tsatsanis C; Spandidos D A (Reprint)
AUTHOR ADDRESS: Medical School, University of Crete, Heraklion, Crete, Greece**Greece
JOURNAL: Folia Biologica (Prague) 46 (6): p226-232 2000 2000
MEDIUM: print
ISSN: 0015-5500
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Retroviruses are implicated in a series of human and animal tumours such as leukaemias, mammary tumours or skin cancer. The mechanism that they use to induce tumour formation varies. Insertional mutagenesis is a common mechanism in rodent, feline and avian retroviruses, where the %%%retrovirus%%% integrates into the host %%%genome%%% and affects the transcription of the neighbouring genes. Cloning of these affected genes led to identification of a series of oncogenes that play a significant role in the induction of human neoplasms. %%%Retrovirus%%% insertion also serves as a model to identify collaborating oncogenes. Human retroviruses use different, more complex mechanisms contributing to oncogenesis. Studies of the propagation and induction mechanisms used by retroviruses have given insight to the understanding of oncogenesis.

9/7/58
DIALOG(R)File 5:Biosis Previews(R)

0012878181 BIOSIS NO.: 200100050020
Endogenous retroviruses and the human germline
AUTHOR: Bock Michael; Stoye Jonathan P (Reprint)
AUTHOR ADDRESS: Division of Virology, National Institute for Medical Research, The Ridgeway, London, NW7 1AA, UK**UK
JOURNAL: Current Opinion in Genetics and Development 10 (6): p651-655 December, 2000 2000
MEDIUM: print
ISSN: 0959-437X
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Citation
LANGUAGE: English

9/7/59
DIALOG(R)File 5:Biosis Previews(R)

0012806666 BIOSIS NO.: 200000524979
The DNA methyltransferases of mammals
AUTHOR: Bestor Timothy H (Reprint)
AUTHOR ADDRESS: Department of Genetics and Development, College of Physicians and Surgeons of Columbia University, 701 West 168th Street, New York, NY, 10032, USA**USA
JOURNAL: Human Molecular Genetics 9 (16): p2395-2402 October, 2000 2000
MEDIUM: print
ISSN: 0964-6906
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The biological significance of 5-methylcytosine was in doubt for many years, but is no longer. Through targeted mutagenesis in mice it has been learnt that every protein shown by biochemical tests to be involved in the establishment, maintenance or interpretation of genomic methylation patterns is encoded by an essential gene. A human genetic disorder (ICF syndrome) has recently been shown to be caused by mutations in the DNA methyltransferase 3B (DNMT3B) gene. A second human disorder (Rett syndrome) has been found to result from mutations in the MECP2 gene, which encodes a protein that binds to methylated DNA. Global

%%%genome%%% demethylation caused by targeted mutations in the DNA methyltransferase-1 (Dnmt1) gene has shown that cytosine methylation plays essential roles in X-inactivation, genomic imprinting and %%%genome%%% stabilization. The majority of genomic 5-methylcytosine is now known to enforce the transcriptional silence of the enormous burden of transposons and retroviruses that have accumulated in the mammalian %%%genome%%%. It has also become clear that programmed changes in methylation patterns are less important in the regulation of mammalian development than was previously believed. Although a number of outstanding questions have yet to be answered (one of these questions involves the nature of the cues that designate sites for methylation at particular stages of gametogenesis and early development), studies of DNA methyltransferases are likely to provide further insights into the biological functions of genomic methylation patterns.

9/7/60
DIALOG(R)File 5:Biosis Previews(R)

0012700232 BIOSIS NO.: 200000418545
Lentivirus replication and regulation
BOOK TITLE: Annual %%%Review%%% of Genetics
AUTHOR: Tang Hengli (Reprint); Kuhen Kelli L (Reprint); Wong-Staal Flossie (Reprint)
BOOK AUTHOR/EDITOR: Campbell Allan; Anderson Wyatt W; Jones Elizabeth W
AUTHOR ADDRESS: Department of Medicine and Biology, University of California, San Diego, CA, 92093-0665, USA**USA
SERIES TITLE: Annual %%%Review%%% of Genetics 33 p133-170 1999
MEDIUM: print
BOOK PUBLISHER: Annual Reviews {a}, 4139 El Camino Way, Palo Alto, CA, 94303-0139, USA
ISSN: 0066-4197 ISBN: 0-8243-1233-3 (cloth)
DOCUMENT TYPE: Book; Book Chapter
RECORD TYPE: Citation
LANGUAGE: English

9/7/61
DIALOG(R)File 5:Biosis Previews(R)

0012658466 BIOSIS NO.: 200000376779
In the beginning: %%%Genome%%% recognition, RNA encapsidation and the initiation of complex %%%retrovirus%%% assembly
AUTHOR: Jewell Nancy A; Mansky Louis M (Reprint)
AUTHOR ADDRESS: Department of Molecular Virology, Immunology, and Medical Genetics, Center for Retrovirus Research, and Comprehensive Cancer Center, Ohio State University Medical Center, 333 West 10th Ave, 2078 Graves Hall, Columbus, OH, 43210, USA**USA
JOURNAL: Journal of General Virology 81 (8): p1889-1899 August, 2000 2000
MEDIUM: print
ISSN: 0022-1317
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Citation
LANGUAGE: English

9/7/62
DIALOG(R)File 5:Biosis Previews(R)

0012506216 BIOSIS NO.: 200000224529
Targeting of the renin-angiotensin system by antisense gene therapy: A possible strategy for the long-term control of hypertension
AUTHOR: Raizada Mohan K (Reprint); Francis Sharon C; Wang Hongwei; Gelband Craig H; Reaves Phyllis Y; Katovich Michael J
AUTHOR ADDRESS: Department of Physiology, University of Florida, Gainesville, FL, 32610-0274, USA**USA
JOURNAL: Journal of Hypertension 18 (4): p353-362 April, 2000 2000
MEDIUM: print

ISSN: 0263-6352
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Traditional pharmacological agents have been successfully used for the treatment of hypertension for a number of decades. However, this therapeutic regimen has reached a conceptual plateau and a cure for the disease is far from appearing on the horizon. With this in mind, and recent advances in state of the art gene delivery system coupled with the anticipated completion of the human %%%genome%%% project, it is timely to think about the possibility of treating and/or curing hypertension using genetic means. In this %%%review%%%, we discuss the role of renin-angiotensin system (RAS) in hypertension; the current gene delivery/gene transfer systems and the RAS as a target for gene therapy to treat hypertension; the successful use of retroviral vectors to deliver antisense to the AT1 receptor (AT1-AS) to prevent the development of hypertension and cardiovascular pathophysiology; the potential use of the viral vectors for the reversal of hypertension; and the future of antisense gene therapy and potential advantages and limitations of this regimen in the treatment and/or control of hypertension.

9/7/63
DIALOG(R)File 5:Biosis Previews(R)

0012472709 BIOSIS NO.: 200000191022
Genetic reassortment and patch repair by recombination in retroviruses
AUTHOR: Mikkelsen Jacob Giehm; Pedersen Finn Skou (Reprint)
AUTHOR ADDRESS: Department of Molecular and Structural Biology, University of Aarhus, C.F. Moellers Alle, Bldg. 130, DK-8000, Aarhus, Denmark** Denmark
JOURNAL: Journal of Biomedical Science 7 (2): p77-99 March-April, 2000
2000
MEDIUM: print
ISSN: 1021-7770
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Retroviral particles contain a diploid RNA %%%genome%%% which serves as template for the synthesis of double-stranded DNA in a complex process guided by virus-encoded reverse transcriptase. The dimeric nature of the %%%genome%%% allows the proceeding polymerase to switch templates during copying of the copackaged RNA molecules, leading to the generation of recombinant proviruses that harbor genetic information derived from both parental RNAs. Template switching abilities of reverse transcriptase facilitate the development of mosaic retroviruses with altered functional properties and thereby contribute to the restoration and evolution of retroviruses facing altering selective forces of their environment. This %%%review%%% focuses on the genetic patchwork of retroviruses and how mixing of sequence patches by recombination may lead to repair in terms of re-established replication and facilitate increased viral fitness, enhanced pathogenic potential, and altered virus tropisms. Endogenous retroelements represent an affluent source of functional viral sequences which may hitchhike with virions and serve as sequence donors in patch repair. We describe here the involvement of endogenous viruses in genetic reassortment and patch repair and %%%review%%% important examples derived from cell culture and animal studies. Moreover, we discuss how the patch repair phenomenon may challenge both safe usage of %%%retrovirus%%%-based gene vehicles in human gene therapy and the use of animal organs as xenografts in humans. Finally, the ongoing mixing of distinct human immunodeficiency virus strains and its implications for antiviral treatment is discussed.

9/7/64
DIALOG(R)File 5:Biosis Previews(R)

0012470395 BIOSIS NO.: 200000188708
Retroviral regulators of gene expression in human %%%genome%%% as possible factors of its evolution
AUTHOR: Sverdlov E D (Reprint)
AUTHOR ADDRESS: Institute of Molecular Genetics, Russian Academy of Sciences, ul. Kurchatova 46, Moscow, 123182, Russia**Russia
JOURNAL: Bioorganicheskaya Khimiya 25 (11): p821-827 Nov., 1999 1999
MEDIUM: print
ISSN: 0132-3423
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: Russian

ABSTRACT: Human endogenous viruses, including their possible role in evolution, are reviewed.

9/7/65
DIALOG(R)File 5:Biosis Previews(R)

0012405856 BIOSIS NO.: 200000124169
Retroviruses and primate evolution
AUTHOR: Sverdlov Eugene D (Reprint)
AUTHOR ADDRESS: Institute of Molecular Genetics RAS, Kurchatov Sq., 123182, Moscow, Russia**Russia
JOURNAL: Bioessays 22 (2): p161-171 Feb., 2000 2000
MEDIUM: print
ISSN: 0265-9247
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Citation
LANGUAGE: English

9/7/66
DIALOG(R)File 5:Biosis Previews(R)

0012263563 BIOSIS NO.: 199900523223
Molecular control of cell cycle progression in primary human hematopoietic stem cells: Methods to increase levels of retroviral-mediated transduction
AUTHOR: Dao M A; Nolta J A (Reprint)
AUTHOR ADDRESS: Division of Research Immunology/Bone Marrow Transplantation, Childrens Hospital of Los Angeles, and Departments of Pediatrics and Craniofacial Developmental Biology, University of Southern California School of Medicine, 4650 Sunset Blvd, Los Angeles, CA, 90027, USA**USA
JOURNAL: Leukemia (Basingstoke) 13 (10): p1473-1480 Oct., 1999 1999
MEDIUM: print
ISSN: 0887-6924
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Pluripotent hematopoietic stem cells (HSC) are the ideal targets for gene transfer because they can repopulate a sublethally irradiated recipient, giving rise to all lineages of blood cells. Thus, introduction of a corrected gene into HSC (stem cell gene therapy) should ensure persistent transmission of the gene. To date, the most efficient mode of gene delivery is via Moloney murine leukemia virus (MoMuLV)-based retroviral vectors which stably integrate into the %%%genome%%% of the target cell. The quiescent nature of HSC and the fact that MoMuLV-based retroviral vectors can only integrate into dividing cells are major obstacles in gene therapy. While increasing efforts have been directed toward identifying growth factors which facilitate division of primary hematopoietic progenitor and stem cells, little is known about the molecular mechanisms which these cells use to enter cell cycle. In this %%%review%%%, we will discuss the correlation between the hematopoietic inhibitory and growth factors and their impact on the regulation of the cell cycle components.

9/7/67
DIALOG(R)File 5:Biosis Previews(R)

0012210744 BIOSIS NO.: 199900470404
Retroviruses: Ancient and modern
AUTHOR: Weiss R A (Reprint); Griffiths D; Takeuchi Y; Patience C; Venables P J W
AUTHOR ADDRESS: Windeyer Institute of Medical Sciences, University College London, 46 Cleveland Street, London, W1P 6DB, UK**UK
JOURNAL: Archives of Virology Supplement 0 (15): p171-177 1999 1999
MEDIUM: print
ISSN: 0939-1983
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Retroviruses are transmitted in two distinct ways: as infectious virions and as 'endogenous' proviral DNA integrated in the germ line of their hosts. Modern infectious viruses such as HIV recently infected mankind from simian hosts, whereas human endogenous retroviral genomes have been present throughout old world primate evolution. Recently we have characterised novel retroviruses in humans and pigs. Human %%%retrovirus%%% 5 (HRV-5) is detected as an exogenous %%%genome%%% in association with arthritis and systemic lupus erythematosus. Porcine endogenous retroviruses (PERV) are carried in swine DNA but can be activated to produce virions that are infectious for human cells, which has implications for xenotransplantation. A brief account of HRV-5 and PERV is given here.

9/7/68
DIALOG(R)File 5:Biosis Previews(R)

0012110640 BIOSIS NO.: 199900370300
General properties of retroviruses
AUTHOR: Rokutanda Makoto (Reprint)
AUTHOR ADDRESS: Department of Microbiology, National Defense Medical College, Tokorozawa, Saitama, 359-8513, Japan**Japan
JOURNAL: Boei Ika Daigakko Zasshi 23 (4): p225-237 Dec., 1998 1998
MEDIUM: print
ISSN: 0385-1796
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: Japanese

ABSTRACT: History of %%%retrovirus%%% research, the general and fundamental characters of retroviruses, and the mechanism of virus replication were described briefly. History of development of %%%retrovirus%%% research is very interesting as history of biological science. Research of molecular biology and cancer research were deeply influenced by discoveries of %%%retrovirus%%% research. The mechanism of %%%retrovirus%%% replication shows unique characteristics compared with other viruses, such as reverse transcription and integration of viral %%%genome%%%.

9/7/69
DIALOG(R)File 5:Biosis Previews(R)

0011905689 BIOSIS NO.: 199900165349
Foamy viruses are unconventional retroviruses
AUTHOR: Linial Maxine L (Reprint)
AUTHOR ADDRESS: Div. Basic Sci., Fred Hutchinson Cancer Res. Cent., 1100 Fairview Ave. N., Seattle, WA 98109, USA**USA
JOURNAL: Journal of Virology 73 (3): p1747-1755 March, 1999 1999
MEDIUM: print
ISSN: 0022-538X

DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Citation
LANGUAGE: English

9/7/70
DIALOG(R)File 5:Biosis Previews(R)

0011701342 BIOSIS NO.: 199800495589
Regional specificity of retroviral integration
AUTHOR: Ryndych A V (Reprint); Zubak S V (Reprint); Tsyba L O (Reprint); Guley N; Lazurkevych Z V (Reprint); Bernardi G
AUTHOR ADDRESS: Inst. Mol. Biol. Genet., Natl. Acad. Sci. Ukr., vul. Zabolotnoho 150, Kyiv 252143, Ukraine**Ukraine
JOURNAL: Biopolimery i Kletka 14 (4): p286-297 July-Aug., 1998 1998
MEDIUM: print
ISSN: 0233-7657
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: Ukrainian

ABSTRACT: The long-help general opinion was that retroviral integration into the cellular %%%genome%%% occurs at random and it is not clear how the local features of integration can be account for the pattern of integration over the whole %%%genome%%%. Using the compositional approach it was shown the viral integration takes place in some regions of the host %%%genome%%% which show a compositional match with viral sequences. This regional specificity of retroviral integration has been demonstrated by: (i) our experimental localization of a number of viral sequences integrated in different compositional genomic compartments; (ii) results from other laboratories concerning the localization of retroviral sequences in open chromatin regions and/or next to CpG islands; (iii) our compositional analysis of genes in the neighborhood of integrated viral sequences. Such conclusion have implications concerning the compositional evolution of retroviral genomes and gene therapy.
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9/7/1
DIALOG(R)File 5:Biosis Previews(R)

0015764960 BIOSIS NO.: 200600110355
Dimer linkage structure in retroviruses: Models that include both duplex and quadruplex domains
AUTHOR: Zarudnaya M I (Reprint); Kolomiets I M; Potyahaylo A L; Hovorun D M
AUTHOR ADDRESS: Natl Acad Sci Ukraine, Inst Mol Biol and Genet, Kiev, Ukraine**Ukraine
AUTHOR E-MAIL ADDRESS: m.i.zarudna@imbg.org.ua
JOURNAL: Ukrainskii Biokhimicheskii Zhurnal 77 (2): p5-15 2005 2005
ISSN: 0201-8470
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: %%%Genome%%% of all known retroviruses consists of two identical molecules of RNA, which are non-covalently linked. The most stable contact site between two RNA molecules is located near their 5' ends. The molecular interactions in the dimer linkage structure (DLS) in mature virions are currently unknown. Recently we suggested that the dimer linkage structure in human immunodeficiency virus I (HIV-1) contains both duplex and quadruplex domains and proposed a model of DLS in HIV-1(Mal) (Central African virus). In this paper we showed that similar models can be also built for HIV-1(Laj), a representative of the North-American and European viruses. One of the double-stranded domains in the model structures represents either an extended duplex formed by different pathways (through base pair melting and subsequent reannealing or by a recombination mechanism) or kissing loop complex. The quadruplexes contain both G- and mixed tetrads, for example, G.C.G.C or A.U.A.U.

Phylogenetic analysis of 350 isolates from NCBI database showed that similar models of DLS are predictable practically for all HIV-1 isolates surveyed. A model of dimer linkage structure in Moloney murine sarcoma virus (MuSV) is also presented. The structure includes a duplex formed by the palindromic sequences and several quadruplexes.

9/7/2
DIALOG(R)File 5:Biosis Previews(R)

0015753047 BIOSIS NO.: 200600098442
Retroviral insertional mutagenesis: past, present and future
AUTHOR: Uren A G; Kool J; Berns A (Reprint); van Lohuizen M
AUTHOR ADDRESS: Netherlands Canc Inst, Div Mol Genet, Plesmanlaan 121, NL-1066 CX Amsterdam, Netherlands**Netherlands
AUTHOR E-MAIL ADDRESS: a.berns@nki.nl; m.v.lohuizen@nki.nl
JOURNAL: Oncogene 24 (52): p7656-7672 NOV 21 2005 2005
ISSN: 0950-9232
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Retroviral insertion mutagenesis screens in mice are powerful tools for efficient identification of oncogenic mutations in an in vivo setting. Many oncogenes identified in these screens have also been shown to play a causal role in the development of human cancers. Sequencing and annotation of the mouse %%%genome%%%, along with recent improvements in insertion site cloning has greatly facilitated identification of oncogenic events in retro-virus-induced tumours. In this %%%review%%%, we discuss the features of retroviral insertion mutagenesis screens, covering the mechanisms by which retroviral insertions mutate cellular genes, the practical aspects of insertion site cloning, the identification and analysis of common insertion sites, and finally we address the potential for use of somatic insertional mutagens in the study of non-haematopoietic and nonmammary tumour types.

9/7/3
DIALOG(R)File 5:Biosis Previews(R)

0015741716 BIOSIS NO.: 200600087111
Intracellular trafficking of retroviral vectors: obstacles and advances
AUTHOR: Anderson J L; Hope T J (Reprint)
AUTHOR ADDRESS: Northwestern Univ, Feinberg Sch Med, Dept Cell and Mol Biol, Chicago, IL 60611 USA**USA
JOURNAL: Gene Therapy 12 (23): p1667-1678 DEC 2005 2005
ISSN: 0969-7128
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Retroviruses are efficient vehicles for delivering transgenes in vivo. Their ability to integrate into the host %%%genome%%%, providing a permanent imprint of their genes in the host, is a key asset for gene therapy. Furthermore, the lentivirus subset of retroviruses can infect nondividing as well as dividing cells. This expands the cell types capable of gene therapy, driving the development of lentiviral vectors. However, the precise mechanisms used by different retroviruses to efficiently deliver their genes into cell nuclei remains largely unclear. Understanding these molecular mechanisms may reveal features to improve the efficacy of current retroviral vectors. Moreover, this knowledge may expose elements pliable to other gene therapy vehicles to improve their in vivo performance and circumvent the biosafety concerns of using retroviral vectors. Therefore, the mechanisms underlying the early trafficking of retroviral vectors in host cells are reviewed here, as understood from studying the native retroviruses. Events after virus entry up to nuclear delivery of the viral cDNA are discussed. Cellular obstacles faced by these retroviral vectors and how they advance beyond these barriers is emphasized.

9/7/4
DIALOG(R)File 5:Biosis Previews(R)

0015727166 BIOSIS NO.: 200600072561
Adaptation, co-evolution, and human susceptibility to HIV-1 infection
AUTHOR: Telenti Amalio (Reprint)
AUTHOR ADDRESS: Univ Lausanne, CHU Vaudois, Inst Microbiol, CH-1011 Lausanne, Switzerland**Switzerland
AUTHOR E-MAIL ADDRESS: amalio.telenti@hospvd.ch
JOURNAL: Infection Genetics and Evolution 5 (4): p327-334 OCT 2005 2005
ISSN: 1567-1348
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Infection with HIV-1, a %%%retrovirus%%% of animal origin, has reached pandemic proportions. For this the virus, characterized by rapid mutation rate, has adapted to the host immunity and to the human cellular environment. Humans are also exerting considerable pressure on HIV- I through the use of antiretroviral agents. On the other hand, long term exposure of humans to other retroviruses and retroelements may have already shaped the human %%%genome%%%. Thus, despite a recent entry of HIV- I in humans, this pathogen might be already exerting evolutionary pressure on humans, by selecting a repertoire of restriction genes and susceptibility loci. (c) 2004 Elsevier B.V. All rights reserved.

9/7/5
DIALOG(R)File 5:Biosis Previews(R)

0015724281 BIOSIS NO.: 200600069676
Hopping around the tumor %%%genome%%%: Transposons for cancer gene discovery
AUTHOR: Collier Lara S; Largaespada David A (Reprint)
AUTHOR ADDRESS: Univ Minnesota Twin Cities, Dept Genet Cell Biol and Dev, Ctr Canc, Arnold and Mabel Beckman Ctr Transposon Res, 6-160 Jackson Hall,321 Church St SE, Minneapolis, MN 55455 USA**USA
AUTHOR E-MAIL ADDRESS: larga002@umn.edu
JOURNAL: Cancer Research 65 (21): p9607-9610 NOV 1 2005 2005
ISSN: 0008-5472
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Retroviruses are powerful insertional somatic mutagens that have been used for many landmark discoveries of cancer genes in model organisms. However, their use as a cancer gene discovery tool has been limited to only a few tissues, mainly the hematopoietic system and mammary gland. Recently, the Sleeping Beauty (SB) transposon system was shown to be useful for random somatic cell mutagenesis in mice, allowing the induction or acceleration of tumor formation both in the hematopoietic system and in sarcomas. in these tumors, SB transposons repeatedly "tagged" specific genes, both known and new cancer genes. These results indicate that the SB system has great potential both for generating specific mouse models of human cancer and for cancer gene discovery in a wide variety of tissues.

9/7/6
DIALOG(R)File 5:Biosis Previews(R)

0015675608 BIOSIS NO.: 200600021003
Silencing and variegation of gammaretrovirus and lentivirus vectors
AUTHOR: Ellis James (Reprint)
AUTHOR ADDRESS: Hosp Sick Children, Dev Biol Program, Room 13-310,TMDT Bldg,101 Coll St, Toronto, ON M5G 1L7, Canada**Canada

AUTHOR E-MAIL ADDRESS: jellis@sickkids.ca
JOURNAL: Human Gene Therapy 16 (11): p1241-1246 NOV 2005 2005
ISSN: 1043-0342
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: %%%Retrovirus%%% vectors integrate into the %%%genome%%%, providing stable gene transfer, but integration contributes in part to transcriptional silencing that compromises long-term expression. In the case of gammaretrovirus vectors based on murine leukemia virus, many integration events are completely silenced in undifferentiated stem cells and in transgenic mice. Gammaretrovirus vectors are also subject to variegation in which sister cells bearing the same provirus differentially express, and cell differentiation can lead to extinction of vector expression. In contrast, lentivirus vectors based on human immunodeficiency virus type 1 appear to express more efficiently, although other reports indicate that lentivirus vectors can be silenced. This %%%review%%% summarizes the key features of gammaretrovirus vector silencing. The evidence for and against gene silencing of lentivirus vectors is described with special emphasis on the potential effects of vector design, provirus copy number, and integration site preferences on silencing. This analysis suggests that the difference between self-inactivating (SIN) lentivirus vectors and their modified SIN gammaretrovirus counterparts may be less dramatic than previously thought. It will therefore be important to further characterize the mechanisms of silencing, in order to create better gammaretrovirus and lentivirus vectors that consistently express at single copy for gene therapy.

9/7/7
DIALOG(R)File 5:Biosis Previews(R)

0015642280 BIOSIS NO.: 200510336780
Transposon tools and methods in zebrafish
AUTHOR: Kawakami Koichi (Reprint)
AUTHOR ADDRESS: Natl Inst Genet, Div Mol and Dev Biol, 1111 Yata, Mishima, Shizuoka 4118540, Japan**Japan
AUTHOR E-MAIL ADDRESS: kokawaka@lab.nig.ac.jp
JOURNAL: Developmental Dynamics 234 (2): p244-254 OCT 2005 2005
ISSN: 1058-8388
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Zebrafish is an excellent model animal to study vertebrate development by genetic approaches. Hundreds of mutations affecting various processes of development have been isolated by chemical mutagenesis and insertional mutagenesis using a pseudotyped %%%retrovirus%%%. However, useful transposon tools and methods had not been available in zebrafish. This is mainly because no active transposable element has been found from the zebrafish %%%genome%%%. Recently, efficient transgenesis, gene trap, and enhancer trap methods have been developed in zebrafish by using the Tol1 and the Sleeping Beauty transposon systems. These methods should increase the usefulness of zebrafish as a model vertebrate and facilitate the study of developmental biology, genetics, and genomics.

9/7/8
DIALOG(R)File 5:Biosis Previews(R)

0015571753 BIOSIS NO.: 200510266253
Targeted modification of mammalian genomes
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JOURNAL: Biotechnology Advances 23 (7-8): p431-469 NOV 2005 2005

ISSN: 0734-9750
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The stable and site-specific modification of mammalian genomes has a variety of applications in biomedicine and biotechnology. Here we outline two alternative approaches that can be employed to achieve this goal: homologous recombination (HR) or site-specific recombination. Homologous recombination relies on sequence similarity (or rather identity) of a piece of DNA that is introduced into a host cell and the host %%%genome%%%. In most cell types, the frequency of homologous recombination is markedly lower than the frequency of random integration. Especially in somatic cells, homologous recombination is an extremely rare event. However, recent strategies involving the introduction of DNA double-strand breaks, triplex forming oligonucleotides or adeno-associated virus can increase the frequency of homologous recombination.Site-specific recombination makes use of enzymes (recombinases, transposases, integrases), which catalyse DNA strand exchange between DNA molecules that have only limited sequence homology. The recognition sites of site-specific recombinases (e.g. Cre, Flp or Phi C31 integrase) are usually 30-50 bp. In contrast, retroviral integrases only require a specific dinucleotide sequence to insert the viral cDNA into the host %%%genome%%%. Depending on the individual enzyme, there are either innumerable or very few potential target sites for a particular integrase/recombinase in a mammalian %%%genome%%%. A number of strategies have been utilised successfully to alter the site-specificity of recombinases. Therefore, site-specific recombinases provide an attractive tool for the targeted modification of mammalian genomes. (C) 2005 Elsevier Inc. All rights reserved.

9/7/9
DIALOG(R)File 5:Biosis Previews(R)

0015540159 BIOSIS NO.: 200510234659
Human endogenous retroviruses in the primate lineage and their influence on host genomes
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JOURNAL: Cytogenetic and Genome Research 110 (1-4): p448-456 2005 2005
ISSN: 1424-8581
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Primates emerged about 60 million years ago. Since that time various primate-targeting retrovirases have integrated in the germ line of primate species, and some drifted to fixation. After germ line fixation, continued activity of proviruses resulted in intragenomic spread of so-called endogenous retroviruses (ERVs). Variant ERVs emerged, amplified in the %%%genome%%% and profoundly altered %%%genome%%% structures and potentially functionality. Importantly, ERVs are %%%genome%%% modifiers of exogenous origin. The human %%%genome%%% contains about 8% of sequences of retroviral origin. The human ERVs (HERVs) comprise many distinct families that amplified to copy numbers of up to several thousand. We %%%review%%% here the evolution of several well-characterized HERV families in the human lineage since initial germ line fixation. It is apparent that endogenous retroviruses profoundly affected the genomes of species in the evolutionary lineage leading to Homo sapiens. Copyright (c) 2005 S. Karger AG, Basel.

9/7/10
DIALOG(R)File 5:Biosis Previews(R)

0015531797 BIOSIS NO.: 200510226297

Nuclear import in viral infections
BOOK TITLE: Current Topics in Microbiology and Immunology
AUTHOR: Greber U E (Reprint); Fornerod M
BOOK AUTHOR/EDITOR: Marsh M (Editor)
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SERIES TITLE: CURRENT TOPICS IN MICROBIOLOGY AND IMMUNOLOGY 285 p109-138 2004
BOOK PUBLISHER: SPRINGER-VERLAG BERLIN, HEIDELBERGER PLATZ 3, D-14197 BERLIN, GERMANY
ISSN: 0070-217X_(print) ISBN: 3-540-21430-5 (H)
DOCUMENT TYPE: Book Chapter; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The separation of transcription in the nucleus and translation in the cytoplasm requires nucleo-cytoplasmic exchange of proteins and RNAs. Viruses have evolved strategies to capitalize on the nucleo-cytoplasmic trafficking machinery of the cell. Here, we first discuss the principal mechanisms of receptor-mediated nuclear import of proteinaceous cargo through the nuclear pore complex, the gate keeper of the cell nucleus. We then focus on viral strategies leading to nuclear import of genomes and subgenomic particles. Nucleo-cytoplasmic transport is directly important for those viruses that are replicating in the nucleus, such as DNA tumor viruses and RNA viruses, including parvoviruses, the DNA retroviruses hepadnaviruses, RNA-retrotransposons and retroviruses, adenoviruses, herpesviruses, papovaviruses, and particular negative-sense RNA viruses, such as the orthomyxovirus influenza virus. The viral strategies of nuclear import turn out to be surprisingly diverse. Their investigation continues to give insight into how nucleic acids pass in and out of the nucleus.

9/7/11
DIALOG(R)File 5:Biosis Previews(R)

0015492228 BIOSIS NO.: 200510186728
Gene Therapy Progress and Prospects: Development of improved lentiviral and retroviral vectors - design, biosafety, and production
AUTHOR: Sinn P L; Sauter S L; McCray P B Jr (Reprint)
AUTHOR ADDRESS: Univ Iowa, Coll Med, Dept Pediat, Program Gene Therapy, Iowa City, IA 52242 USA**USA
JOURNAL: Gene Therapy 12 (14): p1089-1098 JUL 2005 2005
ISSN: 0969-7128
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Replication defective vectors derived from simple retroviruses or the more complex genomes of lentiviruses continue to offer the advantages of long-term expression, cell and tissue specific tropism, and large packaging capacity for the delivery of therapeutic genes. The occurrence of adverse events caused by insertional mutagenesis in three patients in a gene therapy trial for X-linked SCID emphasizes the potential for problems in translating this approach to the clinic. Several %%%genome%%% -wide studies of retroviral integration are now providing novel insights into the integration site preferences of different vector classes. We %%%review%%% recent developments in vector design, integration, biosafety, and production.

9/7/12
DIALOG(R)File 5:Biosis Previews(R)

0015473415 BIOSIS NO.: 200510167915
How retroviruses select their genomes
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JOURNAL: Nature Reviews Microbiology 3 (8): p643-655 AUG 2005 2005
ISSN: 1740-1526
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: As retroviruses assemble in infected cells, two copies of their full-length, unspliced RNA genomes are selected for packaging from a cellular milieu that contains a substantial excess of non-viral and spliced viral RNAs. Understanding the molecular details of %%%genome%%% packaging is important for the development of new antiviral strategies and to enhance the efficacy of retroviral vectors used in human gene therapy. Recent studies of viral RNA structure in vitro and in vivo and high-resolution studies of RNA fragments and protein - RNA complexes are helping to unravel the mechanism of %%%genome%%% packaging and providing the first glimpses of the initial stages of %%%retrovirus%%% assembly.

9/7/13
DIALOG(R)File 5:Biosis Previews(R)

0015360031 BIOSIS NO.: 200510054531
Transgenic animals and their impact on the drug discovery industry
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JOURNAL: Drug Discovery Today 10 (11): p757-767 JUN 1 05 2005
ISSN: 1359-6446
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The ability to direct genetic changes at the molecular level has resulted in a revolution in biology. Nowhere has this been more apparent than in the production of transgenic animals. Transgenic technology lies at the junction of several enabling techniques in such diverse fields as embryology, cell biology and molecular genetics. A host of techniques have been used to effect change in gene expression and develop new pharmaceutical and nutraceutical compounds cost-effectively. Scientific advances gained by transgenic capabilities enable further understanding of basic biological pathways and yield insights into how changes in fundamental processes can perturb programmed development or culminate in disease pathogenesis.

9/7/14
DIALOG(R)File 5:Biosis Previews(R)

0015195523 BIOSIS NO.: 200500101436
The vertical transmission of human immunodeficiency virus type 1: Molecular and biological properties of the virus
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JOURNAL: Critical Reviews in Clinical Laboratory Sciences 42 (1): p1-34 2005 2005
MEDIUM: print
ISSN: 1040-8363
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Citation
LANGUAGE: English

9/7/15
DIALOG(R)File 5:Biosis Previews(R)

0015171713 BIOSIS NO.: 200500078778
Herpesvirus/%%%retrovirus%%% chimeric vectors
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JOURNAL: Current Gene Therapy 4 (4): p409-416 December 2004 2004
MEDIUM: print
ISSN: 1566-5232 _(ISSN print)
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Citation
LANGUAGE: English

9/7/16

0015165967 BIOSIS NO.: 200500073032
Xenotransplantation and risks of zoonotic infections
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JOURNAL: Annals of Medicine 36 (7): p504-517 2004 2004
MEDIUM: print
ISSN: 0785-3890
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The shortage of human organs and tissues for transplantation and the advances in immunology of rejection and in genetic engineering have renewed interest in xenotransplantation - the transplantation of animal organs, tissues or cells to humans. Clinical trials have involved the use of nonhuman primate, porcine, and bovine cells/tissues/organs. In recent years, research has focused mainly on pigs as donors (especially, pigs genetically engineered to carry some human genes). One of the major concerns in xenotransplantation is the risk of transmission of animal pathogens, particularly viruses, to recipients and the possible adaptation of such pathogens for human-to-human transmission. Porcine endogenous retroviruses (PERVs) have been of special concern because of their ability to infect human cells and because, at present, they cannot be removed from the source animal's %%%genome%%%. To date, retrospective studies of humans exposed to live porcine cells/tissues have not found evidence of infection with PERV but more extensive research is needed. This article reviews infectious disease risks associated with xenotransplantation, some measures for minimizing that risk, and microbiological diagnostic methods that may be used in the follow-up of xenotrasplant recipients.

9/7/17

0015138428 BIOSIS NO.: 200500045178
Envelope capture by retroviruses
ORIGINAL LANGUAGE TITLE: La capture d'enveloppe par les %%%retrovirus%%%
AUTHOR: Kim Felix J; Manel Nicolas; Battini Jean-Luc; Sitbon Marc (Reprint)
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JOURNAL: M-S (Medecine Sciences) 20 (10): p876-881 October 2004 2004
MEDIUM: print
ISSN: 0767-0974
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract

LANGUAGE: French

ABSTRACT: Retroelement transposition is a major source of diversity in %%%genome%%% evolution. Among the retrotransposable elements, the retroviruses are distinct in that their "transposition" extends from their initial host cells to neighboring cells and organisms. A determining step in the conversion of a retrotransposable element into an infectious %%%retrovirus%%% is the acquisition of on envelope glycoprotein, designated Env. Here, we %%%review%%% some examples of envelope "capture" by mammal retroviruses and provide evidence for such a mechanism by HTLV. This phenomenon may explain the notable conservation of env genes observed between phylogenetically distant retroviruses. Elucidation of these recombination processes should help to clarify retroviral phylogeny, better understand retroviral pathogenesis, and may lead to the identification of new retroelements.

9/7/18
DIALOG(R)File 5:Biosis Previews(R)

0015135256 BIOSIS NO.: 200500042006
Integration target site selection for retroviruses and transposable elements
AUTHOR: Wu X; Burgess S M (Reprint)
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JOURNAL: CMLS Cellular and Molecular Life Sciences 61 (19-20): p2588-2596 October 2004 2004
MEDIUM: print
ISSN: 1420-682X
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: When a %%%retrovirus%%% infects a cell, its RNA %%%genome%%% is reverse transcribed into a double-stranded DNA, which is then permanently integrated into the host chromosome. Integration is one of the essential steps in the retroviral life cycle. Many transposable elements also move around and integrate into the host %%%genome%%% as part of their life cycle, some through RNA intermediates and some through 'cut-and-paste' mechanisms. Integration of retroviruses and transposable elements into 'sensitive areas' of the %%%genome%%% can cause irreparable damage. On the other hand, because of their ability to integrate permanently, and the relatively efficient rates of transgenesis, retroviruses and transposable elements are widely used as gene delivery tools in basic research and gene therapy trials. Recent events in gene therapy treatments for X-linked severe combined immunity deficiencies (X-SCID) have highlighted both the promise and some of the risks involved with utilizing retroviruses. Nine of 11 children were successfully treated for X-SCID using a %%%retrovirus%%% carrying the gene mutated in this disease. However, later two of these children developed leukemias because of retroviral integrations in the putative oncogene LMO2 (1). A third child has also been demonstrated to have an integration in LMO2, but is as of yet nonsymptomatic (2). It is a bit difficult to explain the high frequency of integrations into the same gene using a random model of retroviral integration, and there has been evidence for decades that retroviral integrations may not be random. But the data were somewhat limited in their power to determine the precise nature of the integration biases. The completion of the human %%%genome%%% sequence coupled with sensitive polymerase chain reaction techniques and an ever-decreasing cost of sequencing has given a powerful new tool to the study of integration site selection. In this %%%review%%%, we describe the findings from several recent global surveys of target site selection by retroviruses and transposable elements, and discuss the possible ramifications of these findings to both mechanisms of action and to the use of these elements as gene therapy vectors.

9/7/19
DIALOG(R)File 5:Biosis Previews(R)

0015133591 BIOSIS NO.: 200500040656
A hard way to the nucleus
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JOURNAL: Molecular Medicine (Baltimore) 10 (1-6): p1-5 January 2004 2004
MEDIUM: print
ISSN: 1076-1551
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: As a member of the %%%Retrovirus%%% family, human immunodeficiency virus (HIV), a causative agent of AIDS, replicates by integrating its %%%genome%%% into the host cell's nuclear DNA. However, in contrast to most retroviruses that depend on mitotic dissolution of the nuclear envelope to gain access to the host cell's %%%genome%%%, the HIV pre-integration complex can enter the nucleus of the target cell during the interphase. Such capacity greatly enhances HIV replication and allows the virus to productively infect terminally differentiated nonproliferating cells, such as macrophages. Infection of macrophages is a critical factor in the pathogenesis of diseases caused by HIV-1 and other lentiviruses. The mechanisms responsible for this unusual feature of HIV have enticed researchers since the early 90s, when the first characterization of the HIV-1 pre-integration complex was reported. Several viral factors, including matrix protein, integrase, viral protein R, and central DNA flap, have been proposed as regulators of HIV-1 nuclear import, only to be later shown as nonessential for this process. As a result, after more than a decade of intense research, there is still no consensus on which HIV-1 and cellular proteins control this critical step in HIV-1 replication. In this %%%review%%%, we will discuss recent advances and suggest possible solutions to the controversial issue of HIV-1 nuclear import.

9/7/20

0015119759 BIOSIS NO.: 200500026824
Evolution of RNA viruses: role of selection and genetic drift
ORIGINAL LANGUAGE TITLE: L'evolution des virus a ARN : roles de la selection et de la derive genetique
AUTHOR: Guyader S; Giblot-Ducray D (Reprint)
AUTHOR ADDRESS: Dept Biol, Univ N Carolina, CB 3280,Coker Hall, Chapel Hill, NC, 27599, USA**USA
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JOURNAL: Virologie (Montrouge) 8 (3): p187-198 May 2004 2004
MEDIUM: print
ISSN: 1267-8694 _(ISSN print)
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: French

ABSTRACT: RNA viruses, retroviruses and pararetroviruses, are known for their rapid evolution, because of high mutation rates and short generation times. Replication errors (mutations and imperfect recombinations) generate a great variability. However, selection pressures shape viral populations diversity, by acting at different steps of virus infectious cycle : strategies of %%%genome%%% expression, interactions with host(s) and vector(s) are the targets of selection. Such a selection sorts out genotypes according to their fitness. The second most important parameter acting on viral population diversity, genetic drift, occurs when population effective size is low, which seems to be frequent during host or tissue infection initiation. By contrast to selection, drift is a random, fitness-independent process, which may lead to the fixation of deleterious mutations. Despite their exceptionally high mutation rates, RNA viruses seem to follow classical population

genetics principles, as showed during the last two decades.

9/7/21
DIALOG(R)File 5:Biosis Previews(R)

0015104216 BIOSIS NO.: 200500009464
Factors regulating endogenous retroviral sequences in human and mouse
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JOURNAL: Cytogenetic and Genome Research 105 (2-4): p351-362 2004 2004
MEDIUM: print
ISSN: 1424-8581 _(ISSN print)
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Endogenous retroviruses (ERVs) are stably integrated in the %%%genome%%% of vertebrates and inherited as Mendelian genes. The several human ERV (HERV) families and related elements represent up to 5 - 8% of the DNA of our species. ERVs may be involved in the regulation of adjacent genomic loci, especially promoting the tissue-specific expression of genes; some HERVs may have functional roles, e. g., coding for the placental fusogenic protein, syncytin. This paper reviews the growing evidence about factors that may modulate ERVs, including: cell and tissue types (with special attention to placenta and germ cells), processes related to differentiation and aging, cytokines, agents that disrupt cell functions (e. g., DNA hypomethylating agents) and steroids. Special attention is given to HERVs, due to their possible involvement in autoimmunity and reproduction, as well as altered expression in some cancer types; moreover, different HERV families may deserve specific attention, due to remarkable differences concerning, e. g., expression in tissues. A comparison with factors interacting with murine ERV-related sequences indicates that the mouse may be a useful model for studying some patterns of HERV regulation. Overall, the available evidence identifies the diverse, potential interactions with endogenous or exogenous factors as a promising field for investigating the roles of ERVs in physiology and disease. Copyright (C) 2004 S. Karger AG, Basel.

9/7/22
DIALOG(R)File 5:Biosis Previews(R)

0015099561 BIOSIS NO.: 200500004809
Human endogenous retroviruses: transposable elements with potential?
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JOURNAL: Clinical and Experimental Immunology 138 (1): p1-9 October 2004 2004
MEDIUM: print
ISSN: 0009-9104 _(ISSN print)
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Human endogenous retroviruses (HERVs) are a significant component of a wider family of retroelements that constitute part of the human %%%genome%%%. These viruses, perhaps representative of previous exogenous retroviral infection, have been integrated and passed through successive generations within the germ line. The retention of HERVs and isolated elements, such as long-terminal repeats, could have the potential to harm. In this %%%review%%% we describe HERVs within the context of the family of known transposable elements and survey these viruses in terms of superantigens and molecular mimics. It is entirely possible that these mechanisms provide the potential for undesired immune responses.

9/7/23
DIALOG(R)File 5:Biosis Previews(R)

0015098367 BIOSIS NO.: 200500003615
Equine Infectious Anemia Virus (EIAV): what has HIV's country cousin got to tell us?
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JOURNAL: Veterinary Research (Les Ulis) 35 (4): p485-512 July 2004 2004
MEDIUM: print
ISSN: 0928-4249 _(ISSN print)
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Equine Infectious Anemia Virus (EIAV) is a lentivirus, of the %%%Retrovirus%%% family, with an almost worldwide distribution, infecting equids. It causes a persistent infection characterized by recurring febrile episodes associating viremia, fever, thrombocytopenia, and wasting symptoms. The disease is experimentally reproducible by inoculation of Shetland ponies or horses with EIAV pathogenic strains. Among lentiviruses, EIAV is unique in that, despite a rapid virus replication and antigenic variation, most animals progress from a chronic stage characterized by recurring peaks of viremia and fever to an asymptomatic stage of infection. The inapparent carriers remain infective for life, as demonstrated by experimental transfer of blood to naive animals. The understanding of the correlates of this immune control is of great interest in defining vaccine strategies. Research on EIAV, this "country cousin" of HIV (Human Immunodeficiency Virus), over the last five decades has produced some interesting results on natural immunological control of lentivirus replication and disease and on the nature and role of virus variation in persistence and pathogenesis. These studies are of interest in the context of HIV and efforts to develop a vaccine. This %%%review%%% will focus on some of the most recent results.

9/7/24
DIALOG(R)File 5:Biosis Previews(R)

0015092433 BIOSIS NO.: 200400473662
Retroelements and the human %%%genome%%%: New perspectives on an old relation
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AUTHOR ADDRESS: Robert Koch Inst, Nordufer 20, D-13353, Berlin, Germany** Germany
AUTHOR E-MAIL ADDRESS: bannertn@rki.de
JOURNAL: Proceedings of the National Academy of Sciences of the United States of America 101 (Suppl. 2): p14572-14579 October 5, 2004 2004
MEDIUM: print
ISSN: 0027-8424 _(ISSN print)
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Retroelements constitute a large portion of our genomes. One class of these elements, the human endogenous retroviruses (HERVs), is comprised of remnants of ancient exogenous retroviruses that have gained access to the germ line. After integration, most proviruses have been the subject of numerous amplifications and have suffered extensive deletions and mutations. Nevertheless, HERV-derived transcripts and proteins have been detected in healthy and diseased human tissues, and HERV-K, the youngest, most conserved family, is able to form virus-like particles. Although it is generally accepted that the integration of retroelements can cause significant harm by disrupting or disregulating essential genes, the role of HERV expression in the etiology of malignancies and autoimmune and neurologic diseases remains controversial. In recent

years, striking evidence has accumulated indicating that some proviral sequences and HERV proteins might even serve the needs of the host and are therefore under positive selection. The remarkable progress in the analysis of host genomes has brought to light the significant impact of HERVs and other retroelements on genetic variation, %%%genome%%% evolution, and gene regulation.

9/7/25
DIALOG(R)File 5:Biosis Previews(R)

0014995777 BIOSIS NO.: 200400366566
Dimerization of retroviral RNA genomes: An inseparable pair
AUTHOR: Paillart Jean-Christophe; Shehu-Xhilaga Miranda; Marquet Roland (Reprint); Mak Johnson
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JOURNAL: Nature Reviews Microbiology 2 (6): p461-472 June 2004 2004
MEDIUM: print
ISSN: 1740-1526 _(ISSN print)
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Citation
LANGUAGE: English

9/7/26
DIALOG(R)File 5:Biosis Previews(R)

0014923894 BIOSIS NO.: 200400294651
Onco-Retroviral and lentiviral vector-based gene therapy for hemophilia: Preclinical studies
AUTHOR: Van Damme An; Chuah Marinee K L; Collen Desire; AlandenDriessche Thierry \(Reprint)
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JOURNAL: Seminars in Thrombosis and Hemostasis 30 (2): p185-195 April 2004 2004
MEDIUM: print
ISSN: 0094-6176
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Citation
LANGUAGE: English

9/7/27
DIALOG(R)File 5:Biosis Previews(R)

0014810061 BIOSIS NO.: 200400190818
Somatic transgenesis using retroviral vectors in the chicken embryo.
AUTHOR: Ishii Yasuo; Reese David E; Mikawa Takashi (Reprint)
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JOURNAL: Developmental Dynamics 229 (3): p630-642 March 2004 2004
MEDIUM: print
ISSN: 1058-8388 _(ISSN print)
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The avian embryo is an excellent model system for experimental studies because of its accessibility and ease of microsurgical manipulations. While the complete chicken %%%genome%%% sequence will soon be determined, a comprehensive germ cell transmission-based genetic approach is not available for this animal model. Several techniques of

somatic cell transgenesis have been developed in the lpast decade. Of these, the retroviral shuttle vector system provides both (1) stable integration of exogenous genes into the host cell %%%genome%%%, and (2) constant expression levels in a target cell population over the course of development. This %%%review%%% summarizes retroviral vectors available for the avian model and outlines the uses of retroviral-mediated gene transfer for cell lineage analysis as well as functional studies of genes and proteins in the chick embryo.

9/7/28
DIALOG(R)File 5:Biosis Previews(R)

0014795684 BIOSIS NO.: 200400163025
"In the beginning": Initiation of minus strand DNA synthesis in retroviruses and LTR-containing retrotransposons.
AUTHOR: Le Grice Stuart F J (Reprint)
AUTHOR ADDRESS: Reverse Transcriptase Biochemistry Section, Resistance Mechanisms Laboratory, HIV Drug Resistance Program, National Cancer Institute at Frederick, Frederick, MD, 21702, USA**USA
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JOURNAL: Biochemistry 42 (49): p14349-14355 December 16, 2003 2003
MEDIUM: print
ISSN: 0006-2960 _(ISSN print)
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Sequestering a host-coded tRNA for initiation of minus (-) strand DNA synthesis is central to the reverse transcription cycle of a number of retroviruses and long terminal repeat (LTR) retrotransposons. However, "self-priming" from a hydrolysis product of the viral %%%genome%%% has been observed for the LTR retrotransposon Tf1 and most likely exists for related elements. Furthermore, in contrast to retroviruses, where DNA synthesis is initiated from the 3'-terminus of the cognate tRNA primer, examples are available where nucleotides of the tRNA anticodon domain are complementary to the viral primer binding site (PBS), necessitating internal cleavage of the primer to provide the appropriate 3'-OH for DNA synthesis. Thus, although the ensuing steps of reverse transcription are common to these elements, several variations in which the replication primer is used have been exploited. In addition, the PBS of the viral RNA %%%genome%%% can vary in size from an 11 nt sequence, through a bipartite cis-acting element, to 18 contiguous nucleotides complementary to the 3'-end of the replication primer. These diverse tRNA-viral RNA interactions, and their consequences for initiation of (-) strand DNA synthesis, are the subject of this %%%review%%%.

9/7/29
DIALOG(R)File 5:Biosis Previews(R)

0014764266 BIOSIS NO.: 200400131620
Plant retroviruses: Structure, evolution and future applications.
AUTHOR: Zaki Essam A (Reprint)
AUTHOR ADDRESS: Department of Biological Sciences, Purdue University, 1392 Lilly Hall of Life Sciences, West Lafayette, IN, 47907-1392, USA**USA
AUTHOR E-MAIL ADDRESS: ezaki@purdue.edu
JOURNAL: African Journal of Biotechnology 2 (6 Cited June 6, 2003): p 136-139 June 2003 2003
MEDIUM: online
ISSN: 1684-5315 _(ISSN print)
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Retroelements, which replicate by reverse transcription, have been detected in higher plants, higher animals, fungi, insects and bacteria. They have been classified into viral retroelements, eukaryotic chromosomal non-viral retroelements and bacterial chromosomal

retroelements. Until recently, retroviruses were thought to be restricted to vertebrates. Plant sequencing projects revealed that plant genomes contain retroviral-like sequences. This %%%review%%% aims to address the structure and evolution of plant retroviruses. In addition, it proposes future applications for these important key components of plant genomes.

9/7/30
DIALOG(R)File 5:Biosis Previews(R)

0014750709 BIOSIS NO.: 200400121466
Avian endogenous retroviruses.
AUTHOR: Borisenko L (Reprint)
AUTHOR ADDRESS: Institute of Molecular Biology and Genetics, Ukrainian Academy of Sciences, 150 Zabolotnogo str., 03143, Kiev, Ukraine**Ukraine
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JOURNAL: Folia Biologica (Cracow) 49 (5): p177-182 2003 2003
MEDIUM: print
ISSN: 0015-5497
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Recent data about the diversity of AER, their structure, expression and possible ways of evolution are summarized and analysed in the present %%%review%%%. Additionally, the role of endogenous retroviruses in ontogenesis and pathology is discussed.

9/7/31
DIALOG(R)File 5:Biosis Previews(R)

0014730363 BIOSIS NO.: 200400101120
Existence of host DNA sequences in schistosomes: Horizontal and vertical transmission.
AUTHOR: Imase Atsuko (Reprint); Matsuda Hajime; Irie Yuji; Iwamura Yukio
AUTHOR ADDRESS: Department of Tropical Medicine and Parasitology, Dokkyo University School of Medicine, Tochigi, 321-0293, Japan**Japan
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JOURNAL: Parasitology International 52 (4): p369-373 December 2003 2003
MEDIUM: print
ISSN: 1383-5769
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The localization of repetitive DNA sequences in the mouse %%%genome%%% such as mouse type 2 Alu sequence (B2) and mouse %%%retrovirus%%%-related sequences was shown in the body of adult Schistosoma japonicum and Schistosoma mansoni by applying an in situ PCR and hybridization technique. Using the same method, mouse major histocompatibility complex (MHC) class I sequence was also found in schistosomes. Furthermore, mouse MHC class I sequence and type A retroviral sequence were detected in S. japonicum and S. mansoni cercarial DNA by blot hybridization. These findings indicated that horizontal and vertical transmission of host DNA sequences occurred in schistosomes. The incorporation and propagation of host sequences in schistosomes and the roles played by such host sequences form the focus of this brief %%%review%%%.

9/7/32
DIALOG(R)File 5:Biosis Previews(R)

0014637751 BIOSIS NO.: 200400008508
%%%Retrovirus%%%-mediated gene transfer and expression cloning: Powerful tools in functional genomics.
AUTHOR: Kitamura Toshio (Reprint); Koshino Yuko; Shibata Fumi; Oki

Toshihiko; Nakajima Hideaki; Nosaka Tetsuya; Kumagai Hidetoshi
AUTHOR ADDRESS: Division of Cellular Therapy, The Institute of Medical Science, The University of Tokyo, 4-6-1 Shirokanedai, Minato-ku, Tokyo, 108-8639, Japan**Japan
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JOURNAL: Experimental Hematology (New York) 31 (11): p1007-1014 November 2003 2003
MEDIUM: print
ISSN: 0301-472X _(ISSN print)
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Most of the human %%%genome%%% has now been sequenced and about 30,000 potential open reading frames have been identified, indicating that we use these 30,000 genes to functionally organize our biologic activities. However, functions of many genes are still unknown despite intensive efforts using bioinformatics as well as transgenic and knockout mice. %%%Retrovirus%%%-mediated gene transfer is a powerful tool that can be used to understand gene functions. We have developed a variety of %%%retrovirus%%% vectors and efficient packaging cell lines that have facilitated the development of efficient functional expression cloning methods. In this %%%review%%%, we describe %%%retrovirus%%%-mediated strategies used for investigation of gene functions and function-based screening strategies.

9/7/33
DIALOG(R)File 5:Biosis Previews(R)

0014464170 BIOSIS NO.: 200300432889
The evolution, distribution and diversity of endogenous retroviruses.
AUTHOR: Gifford Robert; Tristem Michael (Reprint)
AUTHOR ADDRESS: Department of Biological Sciences, Imperial College, Silwood Park, Buckhurst Road, Ascot, Berkshire, SL5 7PY, UK**UK
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JOURNAL: Virus Genes 26 (3): p291-315 May 2003 2003
MEDIUM: print
ISSN: 0920-8569 _(ISSN print)
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The retroviral capacity for integration into the host %%%genome%%% can give rise to endogenous retroviruses (ERVs): retroviral sequences that are transmitted vertically as part of the host germ line, within which they may continue to replicate and evolve. ERVs represent both a unique archive of ancient viral sequence information and a dynamic component of host genomes. As such they hold great potential as informative markers for studies of both virus evolution and host %%%genome%%% evolution. Numerous novel ERVs have been described in recent years, particularly as %%%genome%%% sequencing projects have advanced. This %%%review%%% discusses the evolution of ERV lineages, considering the processes by which ERV distribution and diversity is generated. The diversity of ERVs isolated so far is summarised in terms of both their distribution across host taxa, and their relationships to recognised retroviral genera. Finally the relevance of ERVs to studies of %%%genome%%% evolution, host disease and viral ecology is considered, and recent findings discussed.

9/7/34
DIALOG(R)File 5:Biosis Previews(R)

0014454646 BIOSIS NO.: 200300410308
Human T-cell leukemia virus type I and adult T-cell leukemia.
AUTHOR: Matsuoka Masao (Reprint)
AUTHOR ADDRESS: Institute for Virus Research, Kyoto University, Kyoto, 606-8507, Japan**Japan

AUTHOR E-MAIL ADDRESS: mmatsuok@virus.kyoto-u.ac.jp
JOURNAL: Oncogene 22 (33): p5131-5140 11 August, 2003 2003
MEDIUM: print
ISSN: 0950-9232 _(ISSN print)
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Human T-cell leukemia virus type I (HTLV-I) causes adult T-cell leukemia (ATL) in about 5% of carriers after a long latent period. After its infection, HTLV-I promotes the clonal proliferation of HTLV-I infected cells in vivo by actions of encoded viral proteins, including Tax. However, leukemic cells frequently lack the expression of Tax by the genetic and epigenetic changes of HTLV-I provirus, suggesting that Tax is not always necessary after transformation. Alternatively, ATL cells without Tax protein could escape from the host immune system since Tax is the major target of cytotoxic lymphocytes. During the latent period, alterations of host %%%genome%%% accumulate, finally leading to onset of ATL.

9/7/35
DIALOG(R)File 5:Biosis Previews(R)

0014266492 BIOSIS NO.: 200300225211
Do lipid rafts mediate virus assembly and pseudotyping?
AUTHOR: Briggs John A G; Wilk Thomas; Fuller Stephen D (Reprint)
AUTHOR ADDRESS: Division of Structural Biology, Wellcome Trust Centre for Human Genetics, University of Oxford, Roosevelt Drive, Headington, Henry Wellcome Building for Genomic Medicine, Oxford, OX3 7BN, UK**UK
AUTHOR E-MAIL ADDRESS: stephen.fuller@strubi.ox.ac.uk
JOURNAL: Journal of General Virology 84 (4): p757-768 April 2003 2003
MEDIUM: print
ISSN: 0022-1317 _(ISSN print)
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Co-infection of a host cell by two unrelated enveloped viruses can lead to the production of pseudotypes: virions containing the %%%genome%%% of one virus but the envelope proteins of both viruses. The selection of components during virus assembly must therefore be flexible enough to allow the incorporation of unrelated viral membrane proteins, yet specific enough to exclude the bulk of host proteins. This apparent contradiction has been termed the pseudotypic paradox. There is mounting evidence that lipid rafts play a role in the assembly pathway of non-icosahedral, enveloped viruses. Viral components are concentrated initially in localized regions of the plasma membrane via their interaction with lipid raft domains. Lateral interactions of viral structural proteins amplify the changes in local lipid composition which in turn enhance the concentration of viral proteins in the rafts. An affinity for lipid rafts may be the common feature of enveloped virus proteins that leads to the formation of pseudotypes.

9/7/36
DIALOG(R)File 5:Biosis Previews(R)

0014226564 BIOSIS NO.: 200300185283
Latest development in viral vectors for gene therapy.
AUTHOR: Lundstrom Kenneth (Reprint)
AUTHOR ADDRESS: Regulon Inc./BioXtal., Chemin des Croisettes 22, CH-1066, Epalinges, Switzerland**Switzerland
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JOURNAL: Trends in Biotechnology 21 (3): p117-122 March 2003 2003
MEDIUM: print
ISSN: 0167-7799
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Gene therapy includes the application of various viral vectors, which represent most types and families of viruses, suitable for infection of mammalian host cells. Both hereditary diseases and acquired illnesses, such as cancer, can be targeted. Because of the various properties of each viral vector, the definition of their application range depends on factors such as packaging capacity, host range, cell- or tissue-specific targeting, replication competency, %%%genome%%% integration and duration of transgene expression. Recent engineering of modified viral vectors has contributed to improved gene delivery efficacy.

9/7/37
DIALOG(R)File 5:Biosis Previews(R)

0014191522 BIOSIS NO.: 200300150241
Demystified ... Human endogenous retroviruses.
AUTHOR: Nelson P N (Reprint); Carnegie P R; Martin J; Ejtehadi H Davari; Hooley P; Roden D; Rowland-Jones S; Warren P; Astley J; Murray P G
AUTHOR ADDRESS: Molecular Immunology Laboratories, School of Applied Sciences, University of Wolverhampton, Wulfruna Street, Wolverhampton, WV1 1SB, UK**UK
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JOURNAL: Molecular Pathology 56 (1): p11-18 February 2003 2003
MEDIUM: print
ISSN: 1366-8714
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Human endogenous retroviruses (HERVs) are a family of viruses within our %%%genome%%% with similarities to present day exogenous retroviruses. HERVs have been inherited by successive generations and it is possible that some have conferred biological benefits. However, several HERVs have been implicated in certain cancers and autoimmune diseases. This article demystifies these retroviruses by providing an insight into HERVs, their means of classification, and a synopsis of HERVs implicated in cancer and autoimmunity. Furthermore, the biological roles of HERVs are explored.

9/7/38
DIALOG(R)File 5:Biosis Previews(R)

0014172293 BIOSIS NO.: 200300131012
Dictyostelium mobile elements: Strategies to amplify in a compact %%%genome%%%.
AUTHOR: Winckler T (Reprint); Dingermann T; Gloeckner G
AUTHOR ADDRESS: Institut fuer Pharmazeutische Biologie, Biozentrum, Universitaet Frankfurt/M., Marie-Curie-Strasse 9, 60439, Frankfurt am Main, Germany**Germany
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JOURNAL: CMLS Cellular and Molecular Life Sciences 59 (12): p2097-2111 December 2002 2002
MEDIUM: print
ISSN: 1420-682X
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Dictyostelium discoideum is a eukaryotic microorganism that is attractive for the study of fundamental biological phenomena such as cell-cell communication, formation of multicellularity, cell differentiation and morphogenesis. Large-scale sequencing of the D. discoideum %%%genome%%% has provided new insights into evolutionary strategies evolved by transposable elements (TEs) to settle in compact microbial genomes and to maintain active populations over evolutionary

time. The high gene density (about 1 gene/2.6 kb) of the D. discoideum %%%genome%%% leaves limited space for selfish molecular invaders to move and amplify without causing deleterious mutations that eradicate their host. Targeting of transfer RNA (tRNA) gene loci appears to be a generally successful strategy for TEs residing in compact genomes to insert away from coding regions. In D. discoideum, tRNA gene-targeted retrotransposition has evolved independently at least three times by both non-long terminal repeat (LTR) retrotransposons and %%%retrovirus%%%-like LTR retrotransposons. Unlike the nonspecifically inserting D. discoideum TEs, which have a strong tendency to insert into preexisting TE copies and form large and complex clusters near the ends of chromosomes, the tRNA gene-targeted retrotransposons have managed to occupy 75% of the tRNA gene loci spread on chromosome 2 and represent 80% of the TEs recognized on the assembled central 6.5-Mb part of chromosome 2. In this %%%review%%% we update the available information about D. discoideum TEs which emerges both from previous work and current large-scale %%%genome%%% sequencing, with special emphasis on the fact that tRNA genes are principal determinants of retrotransposon insertions into the D. discoideum %%%genome%%%.

9/7/39
DIALOG(R)File 5:Biosis Previews(R)

0014147314 BIOSIS NO.: 200300106033
The history and principles of retroviral vectors.
AUTHOR: Dornburg Ralph (Reprint)
AUTHOR ADDRESS: Division of Infectious Diseases, Thomas Jefferson University, 1020 Locust Street, Suite 329, Philadelphia, PA, 19107, USA** USA
AUTHOR E-MAIL ADDRESS: ralph.dornburg@mail.tju.edu
JOURNAL: Frontiers in Bioscience 8 (Cited January 24, 2003): pd818-835 May 1, 2003 2003
MEDIUM: online
ISSN: 1093-4715 _(ISSN online)
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: %%%Retrovirus%%%-derived gene transfer systems (retroviral vectors) are the most commonly used gene transfer tools in modern biology. They have been used to study various aspects of retroviral replication, the organization and function of oncogenes and other eucaryotic genes, and, recently, to transduce therapeutic genes to cure inborn errors of metabolism, cancer, AIDS, and many other diseases in man. Highly oncogenic retroviruses served as a model for the construction of artificial retroviral gene transfer systems. These viruses carry a non-viral gene in their %%%genome%%% in addition or substituting for viral protein coding sequences. The replication of such defective retroviruses depends on the presence of a wild-type-virus, which supplies all proteins in trans for particle assembly and infection of a new target cell. Thus, highly oncogenic retroviruses can be considered as naturally occurring gene transfer vectors. Following this principle, cell lines have been constructed which express retroviral protein coding sequences from plasmid DNAs and which contain a viral %%%genome%%% in which the protein coding sequences have been replaced with a gene of interest. This article describes the history, principles, and basic building blocks of first and modern %%%retrovirus%%%-derived gene transfer systems.

9/7/40
DIALOG(R)File 5:Biosis Previews(R)

0014144408 BIOSIS NO.: 200300103127
Endogenous retroviruses and human evolution.
AUTHOR: Khodosevich Konstantin (Reprint); Lebedev Yuri; Sverdlov Eugene
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JOURNAL: Comparative and Functional Genomics 3 (6): p494-498 December 2002
2002
MEDIUM: print
ISSN: 1531-6912 _(ISSN print)
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Humans share about 99% of their genomic DNA with chimpanzees and bonobos; thus, the differences between these species are unlikely to be in gene content but could be caused by inherited changes in regulatory systems. Endogenous retroviruses (ERVs) comprise apprx5% of the human %%%genome%%%. The LTRs of ERVs contain many regulatory sequences, such as promoters, enhancers, polyadenylation signals and factor-binding sites. Thus, they can influence the expression of nearby human genes. All known human-specific LTRs belong to the HERV-K (human ERV) family, the most active family in the human %%%genome%%%. It is likely that some of these ERVs could have integrated into regulatory regions of the human %%%genome%%%, and therefore could have had an impact on the expression of adjacent genes, which have consequently contributed to human evolution. This %%%review%%% discusses possible functional consequences of ERV integration in active coding regions.

9/7/41
DIALOG(R)File 5:Biosis Previews(R)

0014140968 BIOSIS NO.: 200300099687
Diabetes gene therapy: Potential and challenges.
AUTHOR: Xu Ruian (Reprint); Li Hua; Tse Lai-yin; Kung Hsiang-Fu; Lu Hongyan ; Lam Karen S L
AUTHOR ADDRESS: Gene Therapy laboratory, IMB, University of Hong Kong, Hong Kong, China**China
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JOURNAL: Current Gene Therapy 3 (1): p65-82 February 2003 2003
MEDIUM: print
ISSN: 1566-5232 _(ISSN print)
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Citation
LANGUAGE: English

9/7/42
DIALOG(R)File 5:Biosis Previews(R)

0014136377 BIOSIS NO.: 200300095096
Encapsidation and transduction of cellular genes by retroviruses.
AUTHOR: Muriaux Delphine; Rein Alan (Reprint)
AUTHOR ADDRESS: HIV Drug Resistance Program, National Cancer Institute-Frederick, P.O. Box B, Frederick, MD, 21702-1201, USA**USA
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JOURNAL: Frontiers in Bioscience 8 (Cited January 3, 2003): pd135-142 January 1, 2003 2003
MEDIUM: online
ISSN: 1093-4715 _(ISSN online)
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Retroviruses normally package their genomic RNA with high fidelity. However, the fidelity is apparently imperfect, since some cellular mRNA is present in standard %%%retrovirus%%% particles. Further, transcripts originating in the 5' LTR of the integrated provirus sometimes extend beyond the 3' end of the provirus, resulting in the production of chimeric RNAs containing both viral and cellular sequences. These RNAs can be exported to the cytoplasm and packaged into assembling virus particles. When such particles infect a new host cell, reverse transcriptase may copy the cellular sequences, as well as viral

sequences, into DNA. In turn, recombinational events during reverse transcription can result in the incorporation of cellular sequences into retroviral genomes. If the cellular sequences encode proteins involved in the control of cell growth, then the high or inappropriate expression of these sequences as part of the retroviral %%%genome%%% may cause the malignant transformation of the infected cell. Viruses of this type, that transduce cellular transforming genes, are known as acute transforming viruses. They can only arise in animals infected with replication-competent retroviruses, and in general cannot produce progeny viruses without replication-competent "helper" viruses. Since they are produced by a complex, multi-step pathway, acute transforming viruses are only generated at very low frequencies.

9/7/43
DIALOG(R)File 5:Biosis Previews(R)

0014077451 BIOSIS NO.: 200300036170
WNT and FGF gene clusters (%%%Review%%%).
AUTHOR: Katoh Masaru (Reprint)
AUTHOR ADDRESS: Genetics and Cell Biology Section, Genetics Division, National Cancer Center Research Institute, Tsukiji 5-chome, Chuo-ku, Tokyo, 104-0045, Japan**Japan
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JOURNAL: International Journal of Oncology 21 (6): p1269-1273 December 2002 2002
MEDIUM: print
ISSN: 1019-6439 _(ISSN print)
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Mouse mammary tumor virus (MMTV) is a %%%retrovirus%%%, activating Wnt genes (Wnt1/int-1, Wnt3/int-4, Wnt10b), Fgf genes (Fgf3/int-2, Fgf4, Fgf8) and other genes (Notch4/int-3, Eif3s6/int-6) due to proviral integration. Among 19 WNT genes, WNT3 and WNT14B genes are clustered in human chromosome 17q21, WNT3A and WNT14 in human chromosome 1q42, WNT10A and WNT6 in human chromosome 2q35, and WNT10B and WNT1 in human chromosome 12q13. Among 22 FGF genes, FGF19, FGF4 and FGF3 genes are clustered in human chromosome 11q13, while FGF23 and FGF6 in human chromosome 12p13. WNT and FGF gene clusters are conserved between the human %%%genome%%% and the mouse %%%genome%%%. Activation of mouse Wnt or Fgf genes due to proviral integration of MMTV occurs in 5 out of 13 clustered genes, and in 1 out of 28 solitary genes (p=0.0033), which clearly indicates that mouse Wnt or Fgf gene clusters are recombination hot spots associated with carcinogenesis. Recombination results in retroviral integration as well as in chromosomal translocation, gene amplification and deletion during carcinogenesis. The CCND1-FGF19-FGF4-FGF3 gene cluster in human chromosome 11q13 is amplified in breast cancer, squamous cell carcinoma of head and neck, and bladder tumors, and is also translocated in parathyroid tumors and B-cell lymphoma. WNT gene clusters on human chromosome 1q42, 2q35, 12q13, and 17q21 as well as FGF gene cluster on human chromosome 12p13 might be amplified or translocated in human cancer just like FGF gene cluster on human chromosome 11q13.

9/7/44
DIALOG(R)File 5:Biosis Previews(R)

0014067813 BIOSIS NO.: 200300026532
Safety considerations in vector development.
AUTHOR: Kappes John C (Reprint); Wu Xiaoyun (Reprint)
AUTHOR ADDRESS: Department of Medicine, University of Alabama at Birmingham, Birmingham, AL, 35294-1150, USA**USA
JOURNAL: Somatic Cell and Molecular Genetics 26 (1-6): p147-158 November 2001 2001
MEDIUM: print
ISSN: 0740-7750 _(ISSN print)

DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The inadvertent production of replication competent %%%retrovirus%%% (RCR) constitutes the principal safety concern for the use of lentiviral vectors in human clinical protocols. Because of limitations in animal models to evaluate lentiviral vectors for their potential to recombine and induce disease, the vector design itself should ensure against the emergence of RCR in vivo. Issues related to RCR generation and one approach to dealing with this problem are discussed in this chapter. To assess the risk of generating RCR, a highly sensitive biological assay was developed to specifically detect vector recombination in transduced cells. Analysis of lentiviral vector stocks has shown that recombination occurs during reverse transcription in primary target cells. Rejoining of viral protein-coding sequences of the packaging construct and cis-acting sequences of the vector was demonstrated to generate env-minus recombinants (LTR-gag-pol-LTR). Mobilization of recombinant lentiviral genomes was also demonstrated but was dependent on pseudotyping of the vector core with an exogenous envelope protein. 5' sequence analysis has demonstrated that recombinants consist of U3, R, U5, and the PSI packaging signal joined with an open gag coding region. Analysis of the 3' end has mapped the point of vector recombination to the poly(A) tract of the packaging construct's mRNA. The state-of-the-art third generation packaging construct and SIN vector also have been shown to generate env-minus proviral recombinants capable of mobilizing retroviral DNA when pseudotyped with an exogenous envelope protein. A new class of HIV-based vector (trans-vector) was recently developed that splits the gag-pol component of the packaging construct into two parts: one that express Gag/Gag-Pro and another that expresses Pol (RT and IN) fused with Vpr. Unlike other lentiviral vectors, the trans-vector has not been shown to form recombinants capable of DNA mobilization. These results indicate the trans-vector design prevents the generation of env-minus recombinant lentivirus containing a functional gag-pol structure (LTR-gag-pol-LTR), which is absolutely required for retroviral DNA mobilization and the emergence of RCR. Quality assurance based on monitoring for RCR may have limitations as a predictor of safety in vivo, especially in the long term. The demonstration of lentivirus infection via alternative entry mechanisms supports this notion. Therefore, the approach of the possible emergence of RCR in vivo should represent a significant advancement in vector safety quality assurance.

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DIALOG(R)File 5:Biosis Previews(R)

0013997097 BIOSIS NO.: 200200590608
Drosophila germline invasion by the endogenous %%%retrovirus%%% gypsy: Involvement of the viral env gene
AUTHOR: Pelisson A (Reprint); Mejlumian L; Robert V; Terzian C; Bucheton A
AUTHOR ADDRESS: I.G.H. du CNRS (UPR 1142), 141 Rue de la Cardonille, 34396, Montpellier Cedex 5, France**France
JOURNAL: Insect Biochemistry and Molecular Biology 32 (10): p1249-1256 October, 2002 2002
MEDIUM: print
ISSN: 0965-1748
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The endogenous %%%retrovirus%%% gypsy is expressed at high levels in mutant flamenco female flies. Gypsy viral particles extracted from such flies can infect naive flamenco individuals raised in the presence of these extracts mixed into their food. This results in the integration of new proviruses into the germline %%%genome%%%. These proviruses can then increase their copy number by (1) expression in the flamenco female somatic cells, (2) transfer into the oocyte and (3) integration into the %%%genome%%% of the progeny. Surprisingly, unlike the infection observed in the feeding experiments, this strategy of endogenous proviral multiplication does not seem to involve the expression of the viral env

gene.

9/7/46
DIALOG(R)File 5:Biosis Previews(R)

0013895820 BIOSIS NO.: 200200489331
Viruses as gene delivery vectors: Application to gene function, target validation, and assay development
AUTHOR: Lotze Michael T (Reprint); Kost Thomas A
AUTHOR ADDRESS: Molecular Genetics and Biochemistry, University of Pittsburgh Cancer Institute, UPMC Health System, W1534 Biomedical Science Tower, Pittsburgh, PA, 15261, USA**USA
JOURNAL: Cancer Gene Therapy 9 (8): p692-699 August, 2002 2002
MEDIUM: print
ISSN: 0929-1903
DOCUMENT TYPE: Meeting; Meeting Report
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: A Biochemical Pharmacology Discussion Group Conference, was held at the headquarters of the New York Academy of Sciences on December 4, 2001 as part of an ongoing series designed to highlight and %%%review%%% areas important to modern drug development (Figure 1). Briefly introduced by Tom Kost (GlaxoSmithKline) and Michael Lotze (University of Pittsburgh), the focus was on the intersection of genomics, proteomics, and now "viromics." The latter term refers to the use of viruses and viral gene transfer to explore the complexity arising from the vast array of new targets available from the human and murine genomes. Indeed, access to large numbers of genes using viral vectors is a key tool for drug discovery and drug delivery. With 38,000 genes identified within the human %%%genome%%%, only 5000 are considered readily druggable. Generating tools such as these to validate targets represents a major part of the armamentarium of the postgenomic scientist. During the last 12 years alone, there have been over 26,000 publications on virus vectors. Many of them have been found useful in target validation, assay development, and evaluation in in vivo models and gene therapy. Thus, there is now an extensive knowledge base for several viral vectors, with unique attributes within each of them providing versatility, efficiency, and ease of use. The individual scientists presenting at the meeting illustrated many of the unique and useful characteristics of such vector systems including %%%retrovirus%%%, adenovirus, herpes virus, simbis virus, and baculovirus.

9/7/47
DIALOG(R)File 5:Biosis Previews(R)

0013889411 BIOSIS NO.: 200200482922
Damaged DNA and miscounted chromosomes: Human T cell leukemia virus type I Tax oncoprotein and genetic lesions in transformed cells
AUTHOR: Marriott Susan J (Reprint); Lemoine Francene J; Jeang Kuan-Teh
AUTHOR ADDRESS: Department of Molecular Virology and Microbiology, Baylor College of Medicine, One Baylor Plaza, Houston, TX, 77030, USA**USA
JOURNAL: Journal of Biomedical Science 9 (4): p292-298 July-August, 2002 2002
MEDIUM: print
ISSN: 1021-7770
DOCUMENT TYPE: Article; Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Genetic instability is a recurring theme in human cancers. Although the molecular mechanisms mediating this effect commonly observed in transformed cells are not completely understood, it has been proposed to involve either the loss of DNA repair capabilities or the loss of chromosomal stability. The transforming %%%retrovirus%%% human T cell leukemia virus type I (HTLV-I) encodes a viral oncoprotein Tax, which is believed to cause the genomic instability characteristic of

HTLV-I-infected cells. This %%%review%%% focuses on the ability of HTLV-I Tax to disrupt the cellular processes of DNA repair and chromosomal segregation. The consequences of these effects as well as the evolutionary advantage this may provide to HTLV-I are discussed.

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DIALOG(R)File 5:Biosis Previews(R)

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Pig endogenous retroviruses and xenotransplantation
AUTHOR: Blusch Juergen H; Patience Clive; Martin Ulrich (Reprint)
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JOURNAL: Xenotransplantation 9 (4): p242-251 July, 2002 2002
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ABSTRACT: Xenotransplantation of porcine organs might provide an unlimited source of donor organs to treat endstage organ failure diseases in humans. However, pigs harbour retroviruses with unknown pathogenic potential as an integral part of their %%%genome%%%. While until recently the risk of interspecies transmission of these porcine endogenous retroviruses (PERV) during xenotransplantation has been thought to be negligible, several reports on infection of human cells in vitro and spread of PERV from transplanted porcine islets in murine model systems have somewhat challenged this view. Here, we compile available data on PERV biology and diagnostics, and discuss the significance of the results with regard to the safety of clinical xenotransplantation.

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Retroviruses as tools to study the immune system: Commentary
AUTHOR: Lois Carlos; Refaeli Yosef; Qin Xiao-Feng; Van Parijs Luk (Reprint)
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